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# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

|                                 |  |  |
|---------------------------------|--|--|
| Date completed: <u>05-01-03</u> | Search Site                            | Vendors  |
| Searcher: <u>Beverly #4994</u>  | <input type="checkbox"/> STIC          | <input type="checkbox"/> IG Suite                    |
| Terminal time: <u>20</u>        | <input type="checkbox"/> CM-1          | <input type="checkbox"/> STN                         |
| Elapsed time: _____             | <input type="checkbox"/> Pre-S         | <input type="checkbox"/> Dialog                      |
| CPU time: _____                 | Type of Search                         | <input type="checkbox"/> APS                         |
| Total time: <u>23</u>           | <input type="checkbox"/> N.A. Sequence | <input type="checkbox"/> Geninfo                     |
| Number of Searches: _____       | <input type="checkbox"/> A.A. Sequence | <input type="checkbox"/> SDC                         |
| Number of Databases: <u>1</u>   | <input type="checkbox"/> Structure     | <input type="checkbox"/> DARC/Questel                |
|                                 | <input type="checkbox"/> Bibliographic | <input checked="" type="checkbox"/> Other <u>CGN</u> |

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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run On: April 30, 2003, 13:02:10 ; Search time 2934 Seconds  
(without alignments)  
15563.157 Million cell updates/sec

Title: US-09-918-026A-3  
Perfect score: 1569  
Sequence: 1 atggagccaggcggggcccgcg.....cttggctgcctacacctag 1569

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em.sy.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Match | Length | DB | ID         | Description        |
|------------|--------|-------|--------|----|------------|--------------------|
| 1          | 1569   | 100.0 | 1569   | 9  | AF099031   | AF099031 Homo sapi |
| 2          | 1564.2 | 99.7  | 2040   | 9  | AF059203   | AF059203 Homo sapi |
| 3          | 1459   | 93.0  | 2078   | 9  | AF053234   | AF053234 Chlorocob |
| 4          | 1129.6 | 72.0  | 1933   | 10 | AB075946   | AB075946 Rattus no |
| 5          | 1115   | 71.1  | 2170   | 10 | BC025931   | BC025931 Mus muscu |
| 6          | 1112.4 | 70.9  | 1607   | 10 | AF078751   | AF078751 Mus muscu |
| 7          | 421.4  | 26.9  | 3041   | 10 | S81092     | S81092 acyl-coenzy |
| 8          | 421.4  | 26.9  | 3697   | 10 | MUSACACT   | L42293 Mus musculu |
| 9          | 412.2  | 26.3  | 1750   | 10 | D86373     | D86373 Rattus norv |
| 10         | 410.4  | 26.2  | 1673   | 9  | AF053336   | AF053336 Chlorocob |
| 11         | 407.2  | 26.0  | 4011   | 9  | HUMACYLCOA | L21934 Homo sapien |
| 12         | 406.4  | 25.9  | 3024   | 10 | CGU47320   | U47320 Cricetus    |
| 13         | 405.8  | 25.9  | 1528   | 9  | AF354622   | AF354622 Gorilla g |
| 14         | 405.6  | 25.9  | 3407   | 9  | BC028940   | BC028940 Homo sapi |
| 15         | 405.6  | 25.9  | 4011   | 6  | AR053912   | AR053912 Sequence  |
| 16         | 405.6  | 25.9  | 4011   | 6  | AR080271   | AR080271 Sequence  |
| 17         | 405.6  | 25.9  | 4011   | 6  | II17130    | II17130 Sequence 3 |
| 18         | 404    | 25.7  | 1672   | 9  | AF053337   | AF053337 Macaca fa |
| 19         | 404    | 25.7  | 2746   | 9  | AK026611   | AK026611 Homo sapi |
| 20         | 404    | 25.7  | 3425   | 9  | HS804938   | AL833625 Homo sapi |
| 21         | 402.8  | 25.7  | 1528   | 9  | AF354623   | AF354623 Pongo pyg |
| 22         | 359.8  | 22.9  | 4079   | 6  | AR053911   | AR053911 Sequence  |
| 23         | 359.8  | 22.9  | 4079   | 6  | AR080270   | AR080270 Sequence  |
| 24         | 359.8  | 22.9  | 4079   | 6  | II17129    | II17129 Sequence 2 |
| 25         | 268.2  | 17.1  | 295    | 9  | F331502S06 | AF331507 Homo sapi |
| 26         | 268.2  | 17.1  | 11317  | 9  | AF332857S2 | AF332858 Homo sapi |
| 27         | 268.2  | 17.1  | 81364  | 2  | AC021072_3 | Continuation (4 of |
| 28         | 268.2  | 17.1  | 157807 | 9  | AC073573_3 | AC073573 Homo sapi |
| 29         | 268.2  | 17.1  | 193717 | 2  | OC068888   | AC068888 Homo sapi |
| 30         | 194.6  | 12.4  | 919    | 4  | OC065393   | U65393 Oryctolagus |
| 31         | 173.8  | 11.1  | 163811 | 2  | AC110347   | AC110347 Rattus no |
| 32         | 172    | 11.0  | 74310  | 2  | AC013041   | AC013041 Drosophil |
| 33         | 172    | 11.0  | 167467 | 3  | AC009512   | AC009512 Drosophil |
| 34         | 172    | 11.0  | 186322 | 3  | AC008314   | AC008314 Drosophil |
| 35         | 172    | 11.0  | 242566 | 3  | AE003680   | AE003680 Drosophil |
| 36         | 171    | 10.9  | 2102   | 3  | AY113537   | AY113537 Drosophil |
| 37         | 169    | 10.8  | 156297 | 2  | AC123791   | AC123791 Mus muscu |
| 38         | 150.4  | 9.6   | 176    | 9  | F331502S14 | AF331515 Homo sapi |
| 39         | 142.6  | 9.1   | 181870 | 2  | AC024216   | AC024216 Homo sapi |
| 40         | 140.4  | 8.9   | 177    | 9  | F331502S03 | AF331504 Homo sapi |
| 41         | 140.4  | 8.9   | 6458   | 9  | AF332857S1 | AF332857 Homo sapi |
| 42         | 140    | 8.9   | 176    | 9  | F331502S13 | AF331514 Homo sapi |
| 43         | 135    | 8.6   | 170    | 9  | F331502S10 | AF331511 Homo sapi |
| 44         | 134.6  | 8.6   | 996    | 6  | AR053910   | AR053910 Sequence  |
| 45         | 134.6  | 8.6   | 996    | 6  | AR080269   | AR080269 Sequence  |

ALIGNMENTS

RESULT 1  
AF099031  
LOCUS AF099031 1569 bp mRNA linear PRI 11-SEP-2000  
DEFINITION Homo sapiens acyl Co-A: cholesterol acyltransferase-2 (ACAT2) mRNA,  
complete cds.  
ACCESSION AF099031  
VERSION AF099031.2 GI:4878036  
KEYWORDS Homo sapiens.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1569)  
AUTHORS Chang,C.C., Sakashita,N., Ornvold,K., Lee,O., Chang,E.T., Dong,R.,  
Lin,S., Lee,C.Y., Strom,S.C., Kashyap,R., Fung,J.J., Farese,R.V.

|           |   |
|-----------|---|
| TITLE     | Jr., Patoiseau, J.F., Delhon, A. and Chang, T.Y.                    |
| JOURNAL   | Immunological quantitation and localization of ACAT-1 and ACAT-2 in |
| MEDLINE   | human liver and small intestine                                     |
| PUBMED    | J. Biol. Chem. 275 (36), 28083-28092 (2000)                         |
| REFERENCE | 20428724  |
| AUTHORS   | 10846185  |
| TITLE     | 2 (bases 1 to 1569)   |
| JOURNAL   | Lee, O., Farese, R.V. Jr. and Chang, T.Y.                           |
| REFERENCE | Human ACAT-2 nucleotide sequence                                    |
| AUTHORS   | Unpublished   |
| TITLE     | 3 (bases 1 to 1569)   |
| JOURNAL   | Lee, O., Farese, R.V. Jr. and Chang, T.Y.                           |
| REFERENCE | Direct Submission   |
| AUTHORS   | Submitted (15-OCT-1998) Biochemistry, Dartmouth, HB 7200, Hanover,  |
| TITLE     | NH 03755, USA   |
| JOURNAL   | 4 (bases 1 to 1569)   |
| REFERENCE | Lee, O., Farese, R.V. Jr. and Chang, T.Y.                           |
| AUTHORS   | Direct Submission   |
| TITLE     | Submitted (20-MAY-1999) Biochemistry, Dartmouth, HB 7200, Hanover,  |
| JOURNAL   | NH 03755, USA   |
| REMARK    | Sequence update by this sequence                                    |
| COMMENT   | On May 20, 1999 this sequence version replaced qi:3892234.          |

| BASE COUNT | • 276 a | 473 c | 453 g | 367 t |
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| ORIGIN     |         |       |       |       |

| Query Match           | 100.0%          | Score 1569;   | DB 9;   | Length 1569; |
|-----------------------|-----------------|---|---|--------------|
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| Db                    |                 | 1   | ATGAGCCAGGCGGGCCGCTCTCGCTCTGCAGAGGACAGAAAGGCTTGGAGGGGAGCGG  | 60           |
| Qy                    | 61              | GAGGCGCAACCTGTGGAGATGGAAACACTGAGAGGCACAGAGCCCGGACTTGGTACAA    | 120   |              |
| -                     |                 |   |   |              |
| Db                    | 61              | GAGGCGCAACCTGTGGAGATGGAAACACTGAGAGGCACAGAGCCCGGACTTGGTACAA    | 120   |              |
| Qy                    | 121             | TGACCCGACACATGAGGCTGTGAAGGCACAATTTGCTGGAGCAAGCGCAGGCGACAACCTG | 180   |              |
| Db                    | 121             | TGACCCGACACATGAGGCTGTGAAGGCACAATTTGCTGGAGCAAGCGCAGGCGACAACCTG | 180   |              |
| Qy                    | 181             | AGGAGCTGCTGGATCGGGCCATCGGGAGAGCTATACAATCTTACCATCACAGACAAA     | 240   |              |
| Db                    | 181             | AGGAGCTGCTGGATCGGGCCATCGGGAGAGCTATACAATCTTACCATCACAGACAAA     | 240   |              |
| Qy                    | 241             | CCCTGCCCCCACCTCCCCAGGTTCTTGAAGCAGGACCCAGGAGCCATCCCTGGGGAAA    | 300   |              |
| Db                    | 241             | CCCTGCCCCCACCTCCCCAGGTTCTTGAAGCAGGACCCAGGAGCCATCCCTGGGGAAA    | 300   |              |

|    |      |  |      |
|----|------|--|------|
| Qy | 61   | GAGCGCAACCCCTGTGGAGATGAAACACTGAGACGCACAGAGCCCGGACTTGGTACAA     | 120  |
| Db | 112  | GAGCGCAACCCCTGTGGAGATGAAACACTGAGACGCACAGAGCCCGGACTTGGTACAA     | 171  |
| Qy | 121  | TGAGCCGACACATGGAGGCTGTGAAGGCACAATTGCTGGAGCAAGCGCAGGGACAACCTG   | 180  |
| Db | 172  | TGAGCCGACACATGGAGGCTGTGAAGGCACAATTGCTGGAGCAAGCGCAGGGACAACCTG   | 231  |
| Qy | 181  | AGGAGCTGCTGGATGGGCGCATCGCGGAGGCTATACAATCTTACCATCACAAAGACAA     | 240  |
| Db | 232  | AGGAGCTGCTGGATGGGCGCATCGCGGAGGCTATACAATCTTACCATCACAAAGACAA     | 291  |
| Qy | 241  | CTCTGCCCCCACTCTCCCCAGAGTTCTTTGAGCAGCAACCCAGAGGCAATCCCTGGGGAA   | 300  |
| Db | 292  | CTCTGCCCCCACTCTCCCCAGAGTTCTTTGAGCAGCAACCCAGAGGCAATCCCTGGGGAA   | 351  |
| Qy | 301  | CAGAAAGTTTTTCATCTCCCAAGTCCCTGCTTGTATGAGTGAAGCTGACGATTC         | 360  |
| Db | 352  | CAGAAAGTTTTTCATCTCCCAAGTCCCTGCTTGTATGAGTGAAGCTGACGATTC         | 411  |
| Qy | 361  | CGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTTCATCATCAGCACCCCTGGCC   | 420  |
| Db | 412  | CGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTTCATCATCAGCACCCCTGGCC   | 471  |
| Qy | 421  | ATCGACTTTCATGATGAGGCAAGGCTGCTGCTGGAGTTTGAOCTACTGATCTTCAGCTTC   | 480  |
| Db | 472  | ATCGACTTTCATGATGAGGCAAGGCTGCTGCTGGAGTTTGAOCTACTGATCTTCAGCTTC   | 531  |
| Qy | 481  | GGACAGCTGCCATTTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGTCCACCCTGTTGGCG  | 540  |
| Db | 532  | GGACAGCTGCCATTTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGTCCACCCTGTTGGCG  | 591  |
| Qy | 541  | CCGTACCAAGCCCTACGGCTGTGGGCGCAGGGGCAACCTGGACGAGCGCAGGGCCCTGGGC  | 600  |
| Db | 592  | CCGTACCAAGCCCTACGGCTGTGGGCGCAGGGGCAACCTGGACGAGCGCAGGGCCCTGGGC  | 651  |
| Qy | 601  | TGTGCGCTTTTAGCGGCCACGCCGCTGTGTGTCTGTGCGCGTGCCTGACGTGGCCCGTG    | 660  |
| Db | 652  | TGTGCGCTGTAGCGGCCACGCCGCTGTGTGTCTGTGCGCGTGCCTGACGTGGCCCGTG     | 711  |
| Qy | 661  | GAGCATCAGCTCCCGCGGCTCCCGCTGTGCTTGGTCTTCAGAGAGGTTAGGTTCCCTG     | 720  |
| Db | 712  | GAGCATCAGCTCCCGCGGCTCCCGCTGTGCTTGGTCTTCAGAGAGGTTAGGTTCCCTG     | 771  |
| Qy | 721  | ATGAAAGCTACTCTCTCTTGAGAGAGGCTGTGCCCTGGATCTTCCTGCCACAGACGAGT    | 780  |
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| Qy | 781  | GAGGGATCAGCGCCCGCCAGTTTCTCAGCTACTCTACTTCTCTTCTGCCCCAACACTC     | 840  |
| Db | 832  | GAGGGATCAGCGCCCGCCAGTTTCTCAGCTACTCTACTTCTCTCTTCTGCCCCAACACTC   | 891  |
| Qy | 841  | ATCTACAGGAGACTTACCCTAGAGCGCCCTATGTCAGGTGGAAATTATCTGGCCCAAGAC   | 900  |
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| Qy | 901  | TTTGGCCAGGCCCTGGGATGTGTCTCTATGCCCTGCTTCTATCTGGCGCCGCTCTGTGT    | 960  |
| Db | 952  | TTTGGCCAGGCCCTGGGATGTGTCTCTATGCCCTGCTTCTATCTGGCGCCGCTCTGTGT    | 1011 |
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| Db | 1012 | CTGTCTTTGGCCAACTAGCGCGAGCGCCCTTCAGCACCCGTCGCTGTCTCTCTATCT      | 1071 |
| Qy | 1021 | CTGATGCCAGTTGCCAGGCATCTTTCATGCTGCTGCTCATCTTCTTTCCTTCTCTCAT     | 1080 |
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| Qy | 1081 | TGCTGCTCAAGCCCTTTCGCGAGATGCTACGATTTTGAGACAGGAGTGTCTACCGGGAC    | 1144 |
| Db | 1132 | TGCTGCTCAAGCCCTTTCGCGAGATGCTACGATTTTGAGACAGGAGTGTCTACCGGGAC    | 1191 |
| Qy | 1141 | TGTTGGAACCTCAACGTCCTTCTCCAACTACTACCGCACCTTGGAAACGTTGGTCTCATGAC | 1201 |

















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BASE COUNT
ORIGIN

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| Best Local Similarity | 59.2%        | Pred. No. 3.5e-74   |                |             |        |
| Matches 769           | Conservative | 0   | Mismatches 506 | Indels 24   | Gaps 2 |
| QY                    | 287          | CATCCCTGGGAAACAGAAAGTTTTCATCATCCCAAGTCCCTGCTGATGAGCTGATGG   | 346            |             |        |
| DB                    | 1120         | CACCTCAGACACAGGAGAGATTTTATTTCAAGCGACTCTCTTTAGACGAGCTGTTG    | 1179           |             |        |
| QY                    | 347          | AGGTGCAGCATTTCCGCACCATCTACACATGTTTCATCGCTGGCGCTGTGTGCTTTCA  | 406            |             |        |
| DB                    | 1180         | AAGTGGACCATCAGAAACAATTTTACCACATGTTTCATCGCACTCCTCATCCTATTCCG | 1239           |             |        |
| QY                    | 407          | TCAGCACCTTGGCCATCGACTTCATGATGAGCGCAGCTCTGCTGTGAGTTTGACCTAC  | 466            |             |        |
| DB                    | 1240         | TCAGCAGATCGCTGTGGACTACATCGATGAAGAGCGTGGTACTTGAGTTCAATCTCC   | 1299           |             |        |
| QY                    | 467          | TGATCTTCAGCTTCGGACAGCTGCGATTGGCGCTGGTGACCTGGGTGCCATGTTCTGT  | 526            |             |        |
| DB                    | 1300         | TGGCTATGCTTTTGGCAAAATTTCTACTGTATTGGACATGGTGGGCCATGTTCTGT    | 1359           |             |        |
| QY                    | 527          | CCACCTGTTGGCGCGTACCAGGCCCTACGGCTGACGGCTGTGGGCCAGGGG         | 572            |             |        |
| DB                    | 1360         | CTACACTGTCAATCCCCATTTCCTGTTCACGCAATGGCCGACCGTTTACAGCAAGAGTT | 1419           |             |        |
| QY                    | 573          | ---CACCTGACGACGCGACGGCGCTGGCGCTGTCCCTTTTATGCGCCGCCACGCGGTG  | 628            |             |        |
| DB                    | 1420         | CTCACCAATTCATTAATTCCTCTGTCCATGGCTGCTCTCTTAGCTTTCAACTTGGAG   | 1479           |             |        |
| QY                    | 529          | TGCTGTGCGCGCTGCCGTCCACGTGGCGCTGGAGCAATCAGCTCCCGCGCCCTCCCGTT | 688            |             |        |
| DB                    | 1480         | TTCTAGGTTTGTGCCAACATACGTTGTCTTAGCATACACACTGCCACGACCTCCCGGT  | 1539           |             |        |
| QY                    | 689          | GTGTCTCGTCTTCGACGACAGGTAGGTTCTTCATGATAAGTACTCTCTCTGAGAGAG   | 748            |             |        |
| DB                    | 1540         | TCATTCTGATATCGAACACAGATTGGTTGTAATGAAGGCTACACTCAATTTGTCA     | 1599           |             |        |
| QY                    | 749          | CTGTGCTTGGATCTCTCGTCCACAGAGGTGAGGGATCCAGGCC                 | 802            |             |        |
| DB                    | 1600         | ATATCCCACGAGTACTAATCGAGCCACGAGAGAAATCAAGCAAGATCCACTACCCACAG | 1659           |             |        |
| QY                    | 803          | TCTCCAGCTACTCTPACTTCTCTTCTGCCCAACACTCATCTACAGGAGACTTTACCTTA | 862            |             |        |
| DB                    | 1650         | TCAACCACTACTCTPACTTCTCTTCTGTCGCTCACTTATTACGACAACTACCCAA     | 1719           |             |        |

|            |  |
|------------|--|
| RESULT 10  |  |
| AF053336   |  |
| LOCUS      | 1673 bp mRNA linear PRI 12-JUL-1999  |
| DEFINITION | Chlorocebus aethiops acyl-CoA:cholesterol acyltransferase 1 (ACAT1) mRNA, complete cds.                                |
| ACCESSION  | AF053336   |
| VERSION    | AF053336.1   |
| KEYWORDS   | GI:3582756   |
| SOURCE     | Cercopithecus aethiops.  |
| ORGANISM   | Cercopithecus aethiops   |
|            | Cercopithecus aethiops   |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |
|            | Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;   |
|            | Cercopithecinae; Cercopithecus.  |
| REFERENCE  | 1 (bases 1 to 1673)  |
| AUTHORS    | Anderson, R.A., Joyce, C., Davis, M., Reagan, J.W., Clark, M., Shelness, G.S. and Rudel, L.L.                          |
| TITLE      | Identification of a fudel of acyl-CoA:cholesterol acyltransferase specific to liver and intestine in nonhuman primates |
| JOURNAL    | J. Biol. Chem. 273 (41), 26747-26754 (1998)  |
| MEDLINE    | 98434590   |
| PUBMED     | 9756918  |
| REFERENCE  | 2 (bases 1 to 1673)  |
| AUTHORS    | Anderson, R.A., Joyce, C., Davis, M., Reagan, J., Clark, M., Shelness, G. and Rudel, L.L.                              |

TITLE Direct Submission  
 JOURNAL Submitted (11-MAR-1998) Internal Medicine, Wake Forest University  
 School of Medicine, Medical Center Boulevard, Winston-Salem, NC  
 27157, USA

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RESULT 11  
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 VERSION L21934.2 GI:4878021  
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 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 4011)  
 AUTHORS Chang,C.C., Huh,H.Y., Cadigan,K.M. and Chang,T.Y.  
 TITLE Molecular cloning and functional expression of human acyl-coenzyme  
 A:cholesterol acyltransferase cDNA in mutant Chinese hamster ovary  
 cells  
 JOURNAL J. Biol. Chem. 268 (28), 20747-20755 (1993)  
 MEDLINE 94012607



REFERENCE 1 (bases 1 to 3024)  
 AUTHORS Cao, G., Goldstein, J.L. and Brown, M.S.  
 TITLE Complementation of mutation in acyl-CoA:cholesterol acyltransferase (ACAT) fails to restore sterol regulation in ACAT-defective sterol-resistant hamster cells  
 J. Biol. Chem. 271 (24), 14642-14648 (1996).  
 MEDLINE 96278939  
 PUBMED 8662991

REFERENCE 2 (bases 1 to 3024)  
 AUTHORS Cao, G., Brown, M.S. and Goldstein, J.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JAN-1996) Guoqing Cao, Molecular Genetics, University of Texas Southwestern, 5323 Harry Hines Blvd., Dallas, TX 75235, USA

FEATURES  
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RESULT 13

AF354622

LOCUS

DEFINITION

AF354622

AF354622.1

GI:18028941

CODON

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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Gorilla gorilla

Gorilla gorilla

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.

(bases 1 to 1528)

Stautfer,R.L., Walker,A., Ryder,O.A., Lyons-Weiler,M. and

Hedges, S.B.  
Human and ape molecular clocks and constraints on paleontological hypotheses  
J. Hered. 92 (6), 469-474 (2001)  
MEDLINE 21945518  
PUBMED 11948213  
REFERENCE 2 (bases 1 to 1528)  
AUTHORS Hedges, S.B.  
TITLE Direct Submission  
JOURNAL Submitted (27-FEB-2001) Department of Biology, The Pennsylvania State University, 208 Mueller Lab, University Park, PA 16802, USA  
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| Qy | 587 | CGACGGCGCTGGCTGCTGGCTTTTACGCGCGCACCGCTGCTGCTGCTGCTGCTGCTG    | 646 |
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| Db | 682 | TCATCATTTATTCGAGCAGATTCGTTTGTATGAGGAGGCGGCTCATTTGTCAGAGAGA   | 741 |

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| Db | 921  | TTTTTCTATGCTGCTACATCTTTGAAAGGCTTTGTGCCCCCTTGTTCGGAATATCAA     | 980  |
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| Qy | 1282 | CTGGTCTCGCAGTGGCCCATGAGTATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  | 1341 |
| Db | 1281 | GCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG     | 1340 |
| Qy | 1342 | GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG     | 1401 |
| Db | 1341 | GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG     | 1400 |
| Qy | 1402 | CGACCGCGCGCATGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG    | 1461 |
| Db | 1401 | CGGAAAAAGCGATTTGGAATGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG   | 1460 |
| Qy | 1462 | CAGGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG   | 1521 |
| Db | 1461 | TTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG   | 1520 |
| Qy | 1522 | ACTTCT 1528   |      |
| Db | 1521 | ACATTTT 1527  |      |

RESULT 14  
BC028940  
LOCUS  
DEFINITION  
Homo sapiens, sterol O-acyltransferase (acyl-Coenzyme A:  
cholesterol acyltransferase) 1, clone MGC:29940 IMAGE:4991365,  
mRNA, complete cds.  
ACCESSION  
BC028940  
VERSION  
BC028940.1 GI:20809439  
KEYWORDS  
MGC.  
SOURCE  
Homo sapiens.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 3407)  
AUTHORS  
Strausberg, R.  
TITLE  
Direct Submission



JOURNAL

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: AFCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 42 Row: 1 Column: 23  
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES

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/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
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CDS

BASE COUNT 940 a 628 c 681 g 1158 t  
ORIGIN  
Query Match 25.9%; Score 405.6; DB 9; Length 3407;  
Best Local Similarity 58.9%; Pred. No. 5.1e-71;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

|    |     |   |
|----|-----|---|
| QY | 287 | CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGG 346 |
| DB | 404 | CACCTCCAGAACAGAAAGATTTTATGCAAGCGCTCTCTTAGTAGACTGCTTG 463        |
| QY | 347 | AGGTGACGATTTCCGCACCATCTACACATGTTTCATCGTGGCTGCTGTGTTTCATCA 406   |
| DB | 464 | AAGTGGACCATCAGAACAAATATACATGTTTATTTGCCCTCATCTCTTTATCC 523       |
| QY | 407 | TCAGCACCTGGCCATCGACTTCATGATGAGCGAGGCTGCTGCTGGAGTTTGACCTAC 466   |
| DB | 524 | TCAGCACCTGTAGTAGATTCATGATGAGGAGGCTGCTGCTGTTGACCTCAGCTCC 583     |
| QY | 467 | TGATCTTCAGCTTCGGACAGCTGCCATGTCGCTGGTGGTGGTGGTGGTGGTGGTGGT 526   |
| DB | 584 | TGCTTTATGCTTTGGCAATTTCTTACCTACCTGTTGTTGGACCTGGTGGATCATGTTCT 643 |

|    |      |  |
|----|------|--|
| QY | 527  | CCACCTGTTGGCGGTACCAAGCCCTACGGCTGTGGCCAGGGGCACCTGGAACGAGG 586       |
| DB | 644  | CTACATTTTCAGTCCCTATTTTCTGTTTCAACATTTGGCCACTGGCTATACCAAGATT 703     |
| QY | 587  | CGACGGGCTGGGCTGTGGCTTTTAGCGGCCACAGCCGCTGTGCTGCGCGCTGCGGG 646       |
| DB | 704  | CTCATCGCTGATCGTCTCTCTCTTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG 763    |
| QY | 647  | TCG-----ACGTGGCGGTGAGCATCAGCTCCCGCGGCTCCCGTT 688                   |
| DB | 764  | TTCTAGGTTTGGACCAACATATGTTGTTAGCATATACACTGCCACAGCTTCCCGT 823        |
| QY | 689  | GTGCTGCTGCTTCGAGCAGGTAGTCTCTGATGAAAGTACTCTCTCTCTCTCTCTCTCT 748     |
| DB | 824  | TCATCATATATTCGAGCAGATTCGTTTGTATGAAGGCCCATCATTTGTGACAGAGA 883       |
| QY | 749  | CTGTGCTGGGATCTCTCTGTCGACAGAGGTGAGGGGATCCAGGCCCTCCAGTTTCTCA 808     |
| DB | 884  | ACGTGCTGGGTACTAAAT-TCAGTAAGGAGAAATCAAGCACTGTTTCCAAATACCTACA 942    |
| QY | 809  | G-----CTACCTCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 861       |
| DB | 943  | GTCAACAGATTTGACTCTTATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1002    |
| QY | 862  | AGGACGCCCTATGTCAGGTGGAATATGTGGCCAGAACTTTGCCAGGCCCTGGGATGT 921      |
| DB | 1003 | AGGAATCCCACTGTAAGATGGGTTATGCTGCTATGAAGTTTGCACAGGTTCTTTGGTTGC 1062  |
| QY | 922  | GTGCTCTATGCT 981     |
| DB | 1063 | TTTTCTTATGTGACATACATCTTTGAAGCTTTTGGCCCTCTTTTTCGGAATATCAA 1122      |
| QY | 982  | CGAGAGCCCTTCAGCACCCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1041   |
| DB | 1123 | CAGGAGCCCTTCAGCGCTCTGTTCTGCTCTATGTTGTTTAACTCCATCTTTGCCAGGT 1182    |
| QY | 1042 | ATCTTATGCTGCTGCT 1101    |
| DB | 1183 | GTGCTGATCT 1242    |
| QY | 1102 | GAGATGCTACGATTGTGAGACAGATGTTTCTACGGGACTGGTGGAACTCAAGCTCCTTC 1161   |
| DB | 1243 | GAGATGTTAGCTTTGTTGACAGAGATGTTCTATAAGGATTTGTTGGAATCCACGTCTATC 1302  |
| QY | 1162 | TCCAACTACTACCGCACTTGGACGTGGTGGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221 |
| DB | 1303 | TCCAACTATTATAGAACCTGGAATGTTGGTGGTCCATGACTGGCTATATTACTATGCTTAC 1362 |
| QY | 1222 | CAGGATGGGCTGGGCTCTTGGTGGTGGGCGGCGGAGGGGTAGCCATGCTGGGTGCTTC 1281    |
| DB | 1363 | AAGGACTTCTCTGCTGTTTCTCTCCAGAGATTCAAATCTGCTGCTGCTGCTGCTGCTGCT 1422  |
| QY | 1282 | CTGCTCTCCGAGTGGCCCATGATATATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1341  |
| DB | 1423 | GCTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1482  |
| QY | 1342 | GTCATGCTGATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401 |
| DB | 1483 | GTGCTCTCTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542  |
| QY | 1402 | CGACCGGCGCGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATC 1461    |
| DB | 1543 | CGGAAAGCCGATTTGGAATGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1602  |
| QY | 1462 | CAGTCTGACCTGTTACTGCCAGGATGTTGACCGAGGGGCTGCTGCTGCTGCTGCTGCTGCT 1521 |
| DB | 1603 | TTACTCTGCTTTTATCTCAAGAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1662 |
| QY | 1522 | ACTTCTTGGGGCTGGTGCACACCTCGATCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1583  |
| DB | 1663 | ACATTTTGGGATATGCTCCGCGCAGGTTCTCTGGACTTCTGCTGCTGCTGCTGCTGCTGCT 1704 |



Search completed: April 30, 2003, 14:09:08  
Job time : 2957 secs

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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 12:17:55 ; Search time 262 Seconds  
(without alignments)  
13486.204 Million cell updates/sec

Title: US-09-918-026a-3

Perfect score: 1569

Sequence: 1 atggagccagcgggggccg.....cttggtctgccatactag 1569

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

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- 2: /SID22/qcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*
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- 5: /SID22/qcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*
- 6: /SID22/qcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*
- 7: /SID22/qcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*
- 8: /SID22/qcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*
- 9: /SID22/qcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*
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- 23: /SID22/qcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SID22/qcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description                  |
|------------|--------|-------------|--------|----|------------------------------|
| 1          | 1564.2 | 99.7        | 2040   | 21 | AAAT76170 Human ACAT Related |
| 2          | 1425.8 | 90.9        | 1509   | 21 | AAZ57360 Human acyl CoA:cho  |
| 3          | 1112.4 | 70.9        | 1607   | 21 | AAZ57359 Mouse acyl CoA:cho  |
| 4          | 645    | 41.1        | 1082   | 19 | AAV01534 Human acylcoenzyme  |
| 5          | 407.2  | 26.0        | 4011   | 15 | AAQ63212 Acetyl coenzyme A:  |
| 6          | 404    | 25.7        | 3649   | 19 | AAV01536 Human acylcoenzyme  |
| 7          | 394.6  | 25.1        | 3650   | 19 | AAAT96368 Human acyl-coenzym |
| 8          | 191.8  | 12.2        | 455    | 19 | AAV01545 Acylcoenzyme A:cho  |
| 9          | 172    | 11.0        | 1885   | 23 | ABL13759 Drosophila melanog  |

|    |       |      |       |    |           |                    |
|----|-------|------|-------|----|-----------|--------------------|
| 10 | 172   | 11.0 | 2657  | 23 | ABL15694  | Drosophila melanog |
| 11 | 172   | 11.0 | 4260  | 23 | ABL13758  | Drosophila melanog |
| 12 | 134.6 | 8.6  | 996   | 15 | AAQ63210  | Acetyl coenzyme A: |
| 13 | 95    | 6.1  | 983   | 19 | AAV01539  | Human acylcoenzyme |
| 14 | 95    | 6.1  | 993   | 22 | AAO6413   | Human cDNA SEQ ID  |
| 15 | 95    | 6.1  | 1521  | 19 | AAV01533  | Human acylcoenzyme |
| 16 | 95    | 6.1  | 1895  | 21 | AAZ45383  | Human acyl CoA:cho |
| 17 | 95    | 6.1  | 1895  | 21 | AAZ45383  | DNA encoding a pro |
| 18 | 95    | 6.1  | 1976  | 21 | AAAT76169 | Human ACAT Related |
| 19 | 93.8  | 6.0  | 542   | 22 | AAZ57552  | cDNA encoding nove |
| 20 | 92.4  | 5.9  | 774   | 22 | AAZ57244  | cDNA encoding nove |
| 21 | 88.2  | 5.6  | 447   | 21 | AAZ58517  | Human secreted pro |
| 22 | 81.4  | 5.2  | 452   | 24 | ABL181686 | Human ovarian can  |
| 23 | 81.4  | 5.2  | 1650  | 21 | AAZ49452  | Mouse Diacylglycer |
| 24 | 80    | 5.1  | 1122  | 20 | AAZ30335  | DNA encoding a hum |
| 25 | 79.8  | 5.1  | 1766  | 21 | AAZ88846  | Rat acyl CoA:chole |
| 26 | 79.8  | 5.1  | 1766  | 21 | AAZ45385  | Acyl-CoA:cholester |
| 27 | 79.8  | 5.1  | 1766  | 22 | AAZ01105  | Rat sterol acyltra |
| 28 | 70.2  | 4.5  | 1559  | 21 | AAZ48935  | Corn diacylglycer  |
| 29 | 69.6  | 4.4  | 978   | 21 | AAZ48934  | Corn diacylglycer  |
| 30 | 69.6  | 4.4  | 1281  | 21 | AAZ48933  | Corn diacylglycer  |
| 31 | 65    | 4.1  | 901   | 21 | AAZ48936  | Corn diacylglycer  |
| 32 | 64.8  | 4.1  | 1587  | 21 | AAZ48938  | Rice diacylglycer  |
| 33 | 60.6  | 3.9  | 5574  | 24 | AAZ63338  | Chemically pretrea |
| 34 | 60.4  | 3.8  | 1975  | 21 | AAZ48942  | Wheat diacylglycer |
| 35 | 60    | 3.8  | 60    | 24 | ABN36849  | Human spliced tran |
| 36 | 59    | 3.8  | 1942  | 21 | AAZ48939  | Soybean diacylglyc |
| 37 | 55.8  | 3.6  | 4170  | 22 | AAZ69416  | Human immune/haema |
| 38 | 55.4  | 3.5  | 519   | 21 | AAZ88843  | M. alpina acyl COA |
| 39 | 55.4  | 3.5  | 519   | 21 | AAZ45380  | Acyl-CoA:cholester |
| 40 | 55.4  | 3.5  | 519   | 22 | AAZ01319  | Mortierella alpina |
| 41 | 52.8  | 3.4  | 10732 | 21 | AAZ10594  | Gene encoding a su |
| 42 | 50    | 3.2  | 1888  | 21 | AAZ48932  | Arabidopsis diacyl |
| 43 | 50    | 3.2  | 1904  | 21 | AAZ51482  | A. thaliana diacyl |
| 44 | 50    | 3.2  | 1942  | 21 | AAZ88835  | Arabidopsis acyl C |
| 45 | 50    | 3.2  | 1942  | 21 | AAZ45371  | Acyl-CoA:cholester |

ALIGNMENTS

RESULT 1

AAAT76170  
ID AAAT76170 standard; DNA: 2040 BP.

XX AAAT76170;

AC AAAT76170;

XX 14-DEC-2000 (first entry)

XX Human ACAT Related Gene Product 2 ARGP2 coding sequence.

DE Human; ACAT Related Gene Product 2; ARGP2; enzyme;

XX acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1; ACAT2;

KW sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;

XX DGAT; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 52..1620

XX /\*tag= a

XX /product= "Human ARGP2"

XX US6100077-A.

XX PD 08-AUG-2000.

XX PF 01-OCT-1998; 98US-0165042.

XX PR 01-OCT-1998; 98US-0165042.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

PI Sturley SL, Oelkers P;  
XX  
XX WPI; 2000-557622/51.  
DR P-PSDB; AAB21640.  
XX  
XX New nucleic acid encoding a human diacylglycerol acyltransferase,  
PT useful for treating hyperlipidemia, atherosclerosis, heart disease, or  
PT other diseases associated with an imbalance of triglyceride levels -  
XX  
XX Disclosure; Fig 2B; 32pp; English.  
XX  
XX The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) mediates  
CC sterol esterification, an important component of intracellular lipid  
CC homeostasis. The present sequence is the coding sequence of human ACAT  
CC related Gene Product 2 (ARGP2/ ACAT2). The enzyme encoded by the present  
CC sequence is a diacylglycerol acyltransferase (DGAT). ARGP2 esterifies  
CC cholesterol. Also, the activity of ARGP2 is relatively resistant to  
CC histidine active site modifier. ARGP2 is therefore a tissue specific  
CC sterol esterification enzyme.  
XX  
XX Sequence 2040 BP; 389 A; 604 C; 577 G; 470 T; 0 other;  
SQ

Query Match 99.7%; Score 1564.2; DB 21; Length 2040;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 1 ATGGCCAGGGGGCCCGCTGCTGCTGTCAGAGGACAGAAAGGCTGGGAGGGAGCGG 60  
DB 52 ATGGAGCGAGGGGGCCCGCTGCTGCTGTCAGAGGACAGAAAGGCTGGGAGGGAGCGG 111  
QY 61 GAGCGCCAAACCTGTGGAGATGAAACACTGAGACGCACAGAGCCCCGAGCTTGGTACAA 120  
DB 112 GAGCGCCAAACCTGTGGAGATGAAACACTGAGACGCACAGAGCCCCGAGCTTGGTACAA 171  
QY 121 TGGACCGGACACATGAGGCTGTGAAGGCACAAATGCTGGAGCAGCGCAGGGACAACAG 180  
DB 172 TGGACCGGACACATGAGGCTGTGAAGGCACAAATGCTGGAGCAGCGCAGGGACAACAG 231  
QY 181 AGGAGAGCTGCTGGATCGGGCCATCGGGGAGGCTATACAACTCCTACCCATCAAGACAAA 240  
DB 232 AGGAGAGCTGCTGGATCGGGCCATCGGGGAGGCTATACAACTCCTACCCATCAAGACAAA 291  
QY 241 CCTGTGCCCCACCTCCCGAGTTCTTGTAGCAGAGACCAGGAGCCATCCTCTGGGGAAA 300  
DB 292 CCTGTGCCCCACCTCCCGAGTTCTTGTAGCAGAGACCAGGAGCCATCCTCTGGGGAAA 351  
QY 301 CAGAAAGTTTTCATATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGCAGCATTC 360  
DB 352 CAGAAAGTTTTCATATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGCAGCATTC 411  
QY 361 CGCACCATCTACACATGTTTCATCGTGGCCTGTGTGCTTTCATCATCAGCACCCCTGGCC 420  
DB 412 CGCACCATCTACACATGTTTCATCGTGGCCTGTGTGCTTTCATCATCAGCACCCCTGGCC 471  
QY 421 ATCGACTTCATATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 480  
DB 472 ATCGACTTCATATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTC 531  
QY 481 GGACAGCTGCCATTGGCGCTGTGACCTGGGTGCCCATCTTTCTGTCCACCCCTGTGGCG 540  
DB 532 GGACAGCTGCCATTGGCGCTGTGACCTGGGTGCCCATCTTTCTGTCCACCCCTGTGGCG 591  
QY 541 CCGTACCAAGGCCCTTACGGCTGTGGGCCAGGGGCACCTGTGACGACGACGACGGCCCTGGGC 600  
DB 592 CCGTACCAAGGCCCTTACGGCTGTGGGCCAGGGGCACCTGTGACGACGACGACGGCCCTGGGC 651  
QY 601 TGTGGCTTTTAGCGGCCACGCGCTGTGCTCTGCGCGCTCCGGTCCACGTGCCCGTG 660  
DB 652 TGTGGCTTTTAGCGGCCACGCGCTGTGCTCTGCGCGCTCCGGTCCACGTGCCCGTG 711  
QY 661 GAGCATCAGCTCCCGCGGCTCCCGTTGTCTCTGTGCTTTCAGAGAGGTTTAGTTTCTGTG 720  
DB 712 GAGCATCAGCTCCCGCGGCTCCCGTTGTCTCTGTGCTTTCAGAGAGGTTTAGTTTCTGTG 771

KW antilipemic; hypercholesterolaemia; hypertriglyceridaemia;  
KW hyperlipidaemia; ss.  
XX Homo sapiens.

OS

FH Key Location/Qualifiers  
FT CDS 1..1509  
FT /\*tag= a

FT /product= "ACAT-2"  
FT /transl\_except= (pos:571..573,aa:Xaa)  
FT /note= "Xaa is unspecified"

XX W09967368-A1.

XX 29-DEC-1999.

XX 16-JUN-1999; 99WO-US13683.

XX 23-JUN-1999; 98US-0090354.

PR 08-JUN-1999; 98US-0328857.

XX (REGC ) UNIV CALIFORNIA.

PI Cases S, Farese RV, Novak S, Erickson SK;

XX WPI; 2000-106291/09.

DR P-PSDB; AAY67953.

PT Novel polypeptide, useful to treat conditions associated with elevated  
PT cholesterol ester levels e.g. hypercholesterolemia

PS Example; Page 52; 57pp; English.

XX The present sequence encodes the human acyl CoA:cholesterol  
CC acyltransferase designated ACAT-2. ACAT-2 polypeptides can be  
CC administered therapeutically, especially by expressing encoding  
CC polynucleotides, to treat individuals in need of ACAT-2 polypeptide.  
CC They may especially be administered to treat disease conditions  
CC associated with elevated cholesterol ester levels e.g.  
CC hypercholesterolemia or hyperlipidaemia (including  
CC hypertriglyceridaemia), since ACAT-2 catalyses the esterification of  
CC cholesterol with fatty acyl CoA substrates. The polypeptides can also  
CC be used to diagnose diseases related to polypeptide expression or  
CC activity, by analysing for polypeptide presence or amount in a sample.  
CC They are useful to screen for compounds inhibiting or activating the  
CC polypeptide, which can be included in pharmaceutical compositions and  
CC administered therapeutically to treat conditions associated with ACAT-2;  
CC inhibitory agents can especially be used to inhibit ACAT-2 activity,  
CC especially therapeutically, and especially agents which selectively  
CC inhibit ACAT-2 and not prior art ACAT-1.

XX Sequence 1509 BP; 260 A; 457 C; 439 G; 351 T; 2 other;

Query Match 90.9%; Score 1425.8; DB 21; Length 1509;  
Best Local Similarity 95.6%; Pred. No. 0;  
Matches 1500; Conservative 0; Mismatches 9; Indels 60; Gaps 1;

QY 1 ATGGAGCCAGCGGGCCCGCTGCGCTGCGAGAGACAGAGGGCTGGAGGGAGCGG 60

DB 1 ATGGAGCCAGCGGGCCCGCTGCGCTGCGAGAGACAGAGGGCTGGAGGGAGCGG 60

QY 61 GAGCGCCAAACCTGTGGAGATGAACACTGAGACGACAGAGCCCGGACTTGGTACAA 120

DB 61 GAGCGCCAAACCTGTGGAGATGAACACTGAGACGACAGAGCCCGGACTTGGTACAA 120

QY 121 TGGACCCGACATGAGGCTGTGAGGACACATGCTGAGCAAGCGGAGGACAACTG 180

DB 121 TGGACCCGACATGAGGCTGTGAGGACACATGCTGAGCAAGCGGAGGACAACTG 180

QY 181 AGGGAGCTGCTGGATCGGGCCATCGCGGAGGCTATACAACTCTACCCATCACAAGACAA 240

DB 181 AGGGAGCTGCTGGATCGGGCCATCGCGGAGGCTATACAACTCTACCCATCACAAGACAA 240

QY 241 CCTCTGCCCCACCCTCCCGAGGTTCTTGGACGAGACCCAGGACCATCTCCTGGGAAA 300

DB 241 CCTCTGCCCCACCCTCCCGAGGTTCTTGGAGCAG-----TGAGCTGATGGAGGTGAGCATTTTC 360

QY 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTAGACTGATGAGGTGAGCATTTTC 360

DB 276 -----TGAGCTGATGGAGGTGAGCATTTTC 300

QY 361 CGCACCATCTACCATGTTTCATCGCTGGCCTGTGTCTTTCATCATCAGCACCCTGGCC 420

DB 301 CGCACCATCTACCATGTTTCATCGCTGGCCTGTGTCTTTCATCATCAGCACCCTGGCC 360

QY 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGTGGAGTTTGACCTACTGATCTTACGTTTC 480

DB 361 ATCGACTTCATTGATGAGGCGAGGCTGCTGTGGAGTTTGACCTACTGATCTTACGTTTC 420

QY 481 GGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGTCCACCCTTGGGG 540

DB 421 GGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGTCCACCCTTGGGG 480

QY 541 CCGTACCGAGGCTGTAGCGCTGTGGCCAGGGCACCTGTGACGACGAGCGGCGCTGGGC 600

DB 481 CCGTACCGAGGCTGTAGCGCTGTGGCCAGGGCACCTGTGACGACGAGCGGCGCTGGGC 540

QY 601 TGTGCGCTTTTAGCGCCGCCACCGCTGTGTCTGTGCGCGCTGCCGCTCCACGTGGCCGTG 660

DB 541 TGTGCGCTGTAGCGCCGCCACCGCTGTGTCTGTGCGCGCTGCCGCTCCACGTGGCCGTG 600

QY 661 GAGCATCAGCTCCCGCGGCGCTCCCGTGTGTCTGTGCTTTCGAGCAGGTTAGTTCTCTG 720

DB 601 GAGCATCAGCTCCCGCGGCGCTCCCGTGTGTCTGTGCTTTCGAGCAGGTTAGTTCTCTG 660

QY 721 ATGAAAGCTACTCTCTCTGAGAGAGGCTGTGCCCTGGGATCTTCTGCTGCCAGACGAGT 780

DB 661 ATGAAAGCTACTCTCTCTGAGAGAGGCTGTGCCCTGGGATCTTCTGCTGCCAGACGAGT 720

QY 781 GAGGGATCCAGGCGGCGGCTTCTCCAGCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840

DB 721 GAGGGATCCAGGCGGCGGCTTCTCCAGCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780

QY 841 ATCTACAGGAGACTTTACCTTAGGAGCGGCTATGTCAGGTGGAATATGTGGCACAAGAC 900

DB 781 ATCTACAGGAGACTTTACCTTAGGAGCGGCTATGTCAGGTGGAATATGTGGCACAAGAC 840

QY 901 TTTGCCAGGCGCTGGGATGTGTCTTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 960

DB 841 TTTGCCAGGCGCTGGGATGTGTCTTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 900

QY 961 CTTGTCTTTGCCAACAATGAGCGGAGAGCGGCTTTCAGCAGCGGCTGCTGCTCTATC 1020

DB 901 CTTGTCTTTGCCAACAATGAGCGGAGAGCGGCTTTCAGCAGCGGCTGCTGCTCTATC 960

QY 1021 CTGCTGCGCAGCTTGGCAGGAGCTTTCATGCTGCTCTCTCTCTCTCTCTCTCTCTCT 1080

DB 961 CTGCTGCGCAGCTTGGCAGGAGCTTTCATGCTGCTCTCTCTCTCTCTCTCTCTCTCT 1020

QY 1081 TGTGCTCTCAAGCGCTTTCCCGAGAGTGTACGATTTTGAGACAGGATGTTTACCGGGAC 1140

DB 1021 TGTGCTCTCAAGCGCTTTCCCGAGAGTGTACGATTTTGAGACAGGATGTTTACCGGGAC 1080

QY 1141 TGTGGAACCTCAACGCTCTTCTCCAACTACTACCGGCACTTGGAACTGGTGTCCATGAC 1200

DB 1081 TGTGGAACCTCAACGCTCTTCTCCAACTACTACCGGCACTTGGAACTGGTGTCCATGAC 1140

QY 1201 TGTGCTTACAGCTTACCTGTATCAGGATGGCTGCGGCTCTCTTGGTCCCGGGCCGAGG 1260

DB 1141 TGTGCTTACAGCTTACCTGTATCAGGATGGCTGCGGCTCTCTTGGTCCCGGGCCGAGG 1200

QY 1261 GTAGCCATCTGCGGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320

DB 1201 GTAGCCATCTGCGGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260

QY 1321 GTCTGGGGTCTTCTTCTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380











|          |   |  |      |
|----------|---|--|------|
| QY       | 1282  | CTGGTCTCCGAGTGGCCCATGACTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATATCCC      | 1341 |
| Db       | 2756  | GCTGTATCTGCTGTAGTACGAATATGCCCTGGCTGTTGCTTTGCTATATCCC               | 2815 |
| QY       | 1342  | GTCACTGCTGATACACTTCTTCCTTTGTCATTGGAGGAATGTTGAACCTTCATGATGCATGACGAC | 1401 |
| Db       | 2816  | GTGCTGTTTCGTCCTCTCATGCTCTTTTGGAAATGGCTTTCAACTTCATTGTCAATGATAGT     | 2875 |
| QY       | 1402  | CGCACCGCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGAATC          | 1461 |
| Db       | 2876  | CGGAAAAAGCCGATTTGGAATGTTGTGATGTGGACTTCTCTTTTCTTGGCAATGAGATC        | 2935 |
| QY       | 1462  | CAGGTACAGCTGTACTGCCAGGAGTGTGTACGCACGGCGGCACTGCCCTTTACCCAGGCA       | 1521 |
| Db       | 2936  | TTACTCTGCTTTTATTCTCAAGAATGGTATGCACGTGGCACTGCTCTCTGAAAAATCCC        | 2995 |
| QY       | 1522  | ACTTTCTGGGGCTGGTGACACCTCGATCTTGGTCCTGCCAT                          | 1563 |
| Db       | 2996  | ACATTTTGGATTATGTCGGGCCAGGTTCTCGGACTTGTCTG                          | 3037 |
| RESULT 7 |   |  |      |
| AAT96368 |   |  |      |
| ID       | AAT96368 standard; DNA; 3650 BP.                                      |  |      |
| XX       |   |  |      |
| AC       | AAT96368;   |  |      |
| XX       |   |  |      |
| DT       | 21-MAY-1998 (first entry)   |  |      |
| XX       |   |  |      |
| DE       | Human acyl-coenzyme A:cholesterol acyltransferase I DNA.              |  |      |
| XX       |   |  |      |
| KW       | Acyl-coenzyme A: cholesterol acyltransferase I; ACAT; human;          |  |      |
| KW       | sterol; esterification; arteriosclerosis; hyperlipidaemia;            |  |      |
| KW       | antifungal; fungicide; ss.  |  |      |
| XX       |   |  |      |
| OS       | Homo sapiens.   |  |      |
| XX       |   |  |      |
| Key      | Location/Qualifiers   |  |      |
| FT       | 1397..3050  |  |      |
| FT       | /*tag= a  |  |      |
| FT       | /transl_except= (pos:2492..2495, aa:Val)                              |  |      |
| FT       | /note= "this codon has an apparent 1 nucleotide                       |  |      |
| FT       | insertion, which alters the reading                                   |  |      |
| FT       | frame"  |  |      |
| XX       |   |  |      |
| PN       | W09745536-A1.   |  |      |
| XX       |   |  |      |
| PD       | 04-DEC-1997.  |  |      |
| XX       |   |  |      |
| PF       | 30-MAY-1997; 97WO-US09160.  |  |      |
| XX       |   |  |      |
| PR       | 30-MAY-1996; 96US-0657621.  |  |      |
| XX       |   |  |      |
| XX       | * (UYCO ) UNIV COLUMBIA NEW YORK.                                     |  |      |
| PA       | (INDV ) UNIV INDIANA FOUND.   |  |      |
| XX       |   |  |      |
| PI       | Bard M, Sturley SL, Yang H;   |  |      |
| XX       |   |  |      |
| PI       | WPI: 1998-032644/03.  |  |      |
| DR       | P-PSDB; AAW38416.   |  |      |
| XX       |   |  |      |
| PT       | Yeast acyl:coenzyme A:cholesterol acyl:transferase related enzyme I   |  |      |
| PT       | and II - useful to identify inhibitor for treatment of                |  |      |
| PT       | hyperlipidaemia, arteriosclerosis and fungal invasion                 |  |      |
| XX       |   |  |      |
| PS       | Disclosure; Page 61-63; 111pp; English.                               |  |      |
| XX       |   |  |      |
| CC       | This DNA sequence includes a coding region for human macrophage       |  |      |
| CC       | acyl-coenzyme A:cholesterol acyltransferase I (hACAT) (see AAW38416). |  |      |
| CC       | It has been used to search for homologous yeast genes (see AAT96369   |  |      |
| CC       | and AAT96370) and subsequently to identify an additional human        |  |      |
| CC       | isoform (see AAW38421). A novel claimed expression vector (I)         |  |      |

comprises an isolated nucleic acid molecule encoding yeast wild type acyl-coenzyme A:cholesterol acyltransferase 1 (ARE1) (see AAW38417) or 2 (ARE2) (see AAW38418) operatively linked to a promoter. The vector and a claimed host-vector system can be used for the recombinant production of ARE1 or ARE2. The products can be used to identify novel ARE1 or ARE2 inhibitors. ARE2 inhibitors can be used to treat arteriosclerosis or hyperlipidaemia, as well as to inhibit fungal growth or to treat fungal invasion (claimed).

| Query Match           | 25.1%        | Score 394.6  | DB 19          | Length 3650 |      |
|-----------------------|--------------|--|----------------|-------------|------|
| Best Local Similarity | 58.9%        | Pred. No. 3.7e-88  |                |             |      |
| Matches 767           | Conservative | 0  | Mismatches 509 | Indels 27   | Gaps |
| QY                    | 287          | CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCTCTGTATGAGCTGATGG 346        |                |             |      |
| Db                    | 1737         | CACCTCCAGNACAGAAAGATTTTATTGCAAGCGCTCTCTTAGATGAACATGCTTG 1796         |                |             |      |
| QY                    | 347          | AGGTGCAGCATTTCCGACCATCTTACACATGTTTCATCGCTGGCCTGTGTCTTTCATCA 406      |                |             |      |
| Db                    | 1797         | AAGTGGACCACATCAGAAACAATATCATCATGTTTATTGGCCCTCCTCATTTCTTTATCC 1856    |                |             |      |
| QY                    | 407          | TCAGACCCCTGGCCATTCGACTTCATTGATGAGGGCAGGCTGCTCTGGAGTGTGACCTAC 466     |                |             |      |
| Db                    | 1857         | TCAGCACACHTGTAGTAGATTACATTGATGAAGGAAGCTGGTCTTGAGTTCAGCCTCC 1916      |                |             |      |
| QY                    | 467          | TGATCTTCAGCTTTCCGACAGCTGCCAATGGCCCTGGTGACCTGGGTGCCCATGTTCTGT 526     |                |             |      |
| Db                    | 1917         | TGCTTATGCTTTTGGCAAATTTCCCTACCGTTGTTGGACCTGGTGGATCATGTTCCTGT 1976     |                |             |      |
| QY                    | 527          | CCACCTGTTGGCGCGTACCAGGCCCTACGGCCTACGGCTCTGGCCAGGGGACCTCGAACGCAGG 586 |                |             |      |
| Db                    | 1977         | CTACATTTTCAGTTTCCCTATTTTCTGTTTCAACATTTGGGCACATGGCTATAGCAAGATT 2036   |                |             |      |
| QY                    | 587          | CGAGGGCCCTGGGCTGTGCGCTTTTAGCCGCCACGCCCTGGTGCTGTGCGCGTGCCGG 646       |                |             |      |
| Db                    | 2037         | CTCATCGCTGATCGGTTCTCTCTCCATGGGTTCTTTTCATGATCTTCCAGATTGGAG 2096       |                |             |      |
| QY                    | 647          | TCC-----ACGTGGCGGTGGAGCATCAGCTCCCGCGGCGCTCCCGCTCCCGTT 688            |                |             |      |
| Db                    | 2097         | TTCTAGGTTTGGACCAACATATGTTGTGTAGCATATACACTGCCACACAGCTTCCCGGT 2156     |                |             |      |
| QY                    | 689          | GTGTCCTGGCTTCGAGCAGGTTAGTTCCTCATGAAAGCTPACTCTCTCTCGAGAGAGG 748       |                |             |      |
| Db                    | 2157         | TCATCATTAATTGAGCAGATTCGTTTGTATGAAGCCCACTCATTTGTCAGAGAGA 2216         |                |             |      |
| QY                    | 749          | CTGTGCTTGGATCCTTCGTGCCAGCAGAGGTGAGGGATCCAGCCGCCAGTTTCTCCA 808        |                |             |      |
| Db                    | 2217         | ACGTGCCCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCAGCTGTTCCTAATACCTACA 2275 |                |             |      |
| QY                    | 809          | G-----CTACCTCTACTTCTCTCTGCCAACACTCATCTACAGGGAGACTTACCCT 861          |                |             |      |
| Db                    | 2276         | GTCAACACAGTATTGTACTTCTATTGTCCTTACCCTTATCTACCGTGACAGCTATCCC 2335      |                |             |      |
| QY                    | 862          | AGGACGCCCTATGTCAAGTGGAAATATGTGGCCAGAACTTTGCCACGCCCTGGGATGT 921       |                |             |      |
| Db                    | 2336         | AGGAATCCCACTGTAAGATGGGGTATGTGCGCTATGAAGTTTGCACAGCTCTTTGGTTGC 2395    |                |             |      |
| QY                    | 922          | GTGCTCATGCTGCTTCATCCTGGGCCGCTCTGTGTCTCTGTCTTTGCCAACATGAGC 981        |                |             |      |
| Db                    | 2396         | TTTTTCTATGTGTACTACATCTTTGAAAGGCTTTGTGCCCTTGTTCGGAAATATCAA 2455       |                |             |      |
| QY                    | 982          | CGAGAGCCCTTCAGCACCGCTGCCCTGGTCTCTTA-TCCTGCATGCCACGTTGCCAGG 1040      |                |             |      |
| Db                    | 2456         | CAGGAGCCCTTCAGGCCTGCTGCTCTGTCCTATGCGTATTTAACTCCATCTTCCAGG 2515       |                |             |      |
| QY                    | 1041         | CATCTTCATGCTGCTGCTCATCTTCTTTTGGCTTCTCCATGCTGCTCAACGCCTTTGC 1100      |                |             |      |
| Db                    | 2516         | TGTGTGATTCTCTCTCTTACTTTTTTTTGGCTTTTGGACTGCTGCTCAATGSCCTTTGC 2575     |                |             |      |
| QY                    | 1101         | CGAGATGCTACGATTTGGAGACAGATGTTCTACCGGGACTGCTGGAACCTCAACGCTCT 1160     |                |             |      |



CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1885 BP; 410 A; 514 C; 504 G; 457 T; 0 other;

Query Match 11.0%; Score 172; DB 23; Length 1885;  
 Best Local Similarity 51.9%; Pred. No. 8.5e-33;  
 Matches 413; Conservative 0; Mismatches 380; Indels 3; Gaps 1;

QY 774 ACAGAGTGGAGGATCCAGGCCCGCCAGTTTCTCCAGTACCTCTACTTCTCTCTGCCC 833  
 DB 1001 AGGCAGTGGAGGACCTTTTGTCCGCGCTGAGCTGTATACAGTACTTTTGTTCGACC 1060  
 QY 834 AACACTCATCTACAGGAGACTTACCTAGGACGCCCTATGTCCAGTGGGAATATGTGGC 893  
 DB 1061 CACGCTTATCTACCGAGACAGCTACCCGCGACCTCCACATCGCTGGAGTTGGCCT 1120  
 QY 894 CAAGAACTTTGCCAGGCCCTGGGATGTGCTCTATGCTGTCTATGCTGTATCTGCGCCGCT 953  
 DB 1121 GAATCGACTGTGGAGGTGGCCATAGCCTTCTGTACGCGTTCATCCATGAGCGCA 1180  
 QY 954 CTGTGTTCTCTTTCGCAACATGACCGAGAGCCCTTCAGCACCGTCCCTGTGTCT 1013  
 DB 1181 CATCCAGGACACTTCCGACAGTACCGACTGGAACCAATGGGACCTCCAGCTGATCCT 1240  
 QY 1014 CTCTATCTGATCCACGCTTCCAGGACATCTTCATCTGCTGTCTATCTTCTTTCGCTT 1073  
 DB 1241 CAAGCTGTGGCATGTGCTGCCAGCGGGTATCTTCTGTGCGGCTCTACCTAAT 1300  
 QY 1074 CCTCATCTGTGCTCAACGCTTTTGGCGAGTGTACGATTTGGAGACAGGATTTCTA 1133  
 DB 1301 CCTGACTCGTGGTGAATCTACGTCGGAGCTCTACGCTTCGCTGATGAATTTCTA 1360  
 QY 1134 CCGGACTGTGGAACTCAAGCTCTTCTCAACTACTACGCACTTGGAACTGGTGT 1193  
 DB 1361 CAAGACTGTGGAGCTGCGACACTTACGATGGCTACTACAGAACTGGATGCTGCT 1420  
 QY 1194 CCATGACTGGCTTACAGCTACGTATATCAGGATGGCTGCGGCTCCCTTGGTCCCGGC 1253  
 DB 1421 GCAGACTGGCTGAGGATACGTTGTAAGGATATGTACACTCATGTGTCCGAGTTC 1480  
 QY 1254 CGAGGGGTACCATGCTGGTGTGTTCTCTCGCTCCGAGTGGCCCATGATATCTT 1313  
 DB 1481 CAAGTGGCCGCTGCTGGAGTGTTCATGATCTCCGCTGTGTCCATGAGAGTCT 1540  
 QY 1314 CTGCTGCTGCTGGGTTCTTCTATCCGCTCATGCTGATCTCTCTCTGTCATTTGAGG 1373  
 DB 1541 CGGCTTTGCCCTGCAATGTTCTTCCAGTGTATCTTCTTCTTGGGTCGTGGTGT 1600  
 QY 1374 AATGTTGAATTCATGATGATGACAGCCAGCCGCGCCGCGATGGAACGTTGATGTG 1433  
 DB 1601 TGCTTGTGATCTTCTAATGCGAGGTGCTCCAAAGTATG- -GCAACATCTTCTGTG 1657  
 QY 1434 GACCATGCTGTTTACGCGAGGAAATCCAGGTGAGCTGTACTGCGAGGAGTGGTACG 1493  
 DB 1658 GTTCTCTGATCTCTGGGAAATGCGACGCTGATCTCTACATATACGCCATGAGCATACG 1717  
 QY 1494 ACGGCGGACCTGCCCCCTTACCCAGGCAACTTCTGGGGGTGTGTGACACCTCGATCTG 1553  
 DB 1718 CTAAGAACTGCAACCTAAGCAACAGAGTTGGACGTATCGCTGTGCGCGGTATG 1777  
 QY 1554 GTCTTGCCATACCTAG 1569  
 DB 1778 GCGCTGTACAAATTAG 1793

RESULT 10  
 ABL15694  
 ID ABL15694 standard; cDNA; 2657 BP.  
 XX  
 AC ABL15694;

XX 26-MAR-2002 (first entry)  
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 41564.  
 DE  
 XX  
 KW Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX Drosophila melanogaster.  
 XX WO200171042-A2.  
 XX 27-SEP-2001.  
 XX 23-MAR-2001; 2001WO-US09231.  
 XX 23-MAR-2000; 2000US-191637P.  
 XX 11-JUL-2000; 2000US-0614150.  
 XX (PEKE ) PE CORP NY.  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 PI WPI: 2001-656860/75.  
 XX P-PSDB; ABB71591.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX Claim 1; SEQ ID NO 41564; 21pp + Sequence Listing; English.  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72073).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 2657 BP; 704 A; 610 C; 624 G; 719 T; 0 other;

Query Match 11.0%; Score 172; DB 23; Length 2657;  
 Best Local Similarity 51.9%; Pred. No. 9.6e-33;  
 Matches 413; Conservative 0; Mismatches 380; Indels 3; Gaps 1;  
 QY 774 ACAGAGTGGAGGATCCAGGCCCGCCAGTTTCTCCAGTACCTCTACTTCTCTCTGCCC 833  
 DB 185 AGCAGTGGAGGACCTTTTGTCCGCGCTGAGCTGTACAGTACTTTTGTTCGACC 244  
 QY 834 AACACTCATCTACAGGAGACTTACCTAGGAGCCCTATGTCCAGTGGGAATATGTGGC 893  
 DB 245 CACGCTTATCTACCGAGACAGTACCCGCGACCTCCACATCGCTGGAGTTGGCCT 304  
 QY 894 CAAGAACTTTGCCAGGCCCTGGGATGTGCTGTATGCTGTCTATCTCTGCGCCGCT 953  
 DB 305 GAATCGACTGTGGAGGTGGTGGCCATAGCCTTCTCTAGCGGTTTCATCCATGAGCGCA 364  
 QY 954 CTGTGTTCTCTTCCCAACATGAGCGGAGCCCTTCAGCACCCGCTGCTGTGTCT 1013  
 DB 365 CATCCAGGACACTTCGGACAGTACGAGTGGAACTGGGACCTCCAGCTGATCCT 424  
 QY 1014 CTCTATCTGATCCGAGCTTGGCAGGATCTTTCATCTGCTGTCTATCTTCTTGGCCT 1073  
 DB 425 CAAGCTGTTCGGCATGATGTGCTGCCAGCGGCTGATCTTCTGTGCGGCTTACCTAAT 484  
 QY 1074 CCTCCATGTGGCTCAACGCTTTTGGCGAGATCTAGGATTTGGAGACAGGATTTCTA 1133  
 DB 485 CCTGCACTGCTGGCTGAACCTTACGTCGGAGCTGCTACGCTTCGGTGTATGAATGTTCTA 544



RESULT 12  
AAQ63210  
ID AAQ63210 standard; cDNA; 996 BP.  
XX AC  
XX AAQ63210;  
XX  
XX 03-JAN-1995 (first entry)  
XX DT  
XX DE Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).  
XX KW Acetyl coenzyme A: cholesterol acetyltransferase (ACAT); disease;  
XX KW diagnosis; detection; screening; treatment; prophylaxis;  
KW hypercholesterolaemia; atherosclerosis; antisense; probe;  
KW identification; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO9409126-A.  
XX PD 28-APR-1994.  
XX PF 12-OCT-1993; 93WO-US09704.  
XX PR 14-OCT-1992; 92US-0959950.  
XX PR 10-SEP-1993; 93US-0121057.  
XX  
XX PA (DART-) DARTMOUTH COLLEGE.  
XX PI Chang CCY, Chang T;  
XX WP; 1994-151312/18.  
XX  
XX Acetyl coenzyme A: cholesterol acetyltransferase and nucleic  
PT acid sequence encoding it - used to correct enzyme deficiencies  
PT and screen for enzyme inhibitors  
XX  
XX Claim 13; Figure 3; 52pp; English.  
XX  
XX The acetyl coenzyme A: cholesterol acetyltransferase (ACAT) gene  
CC sequence enables the screening of human populations for abnormal  
CC human ACAT activities for disease diagnosis. It provides  
CC information concerning the catalytic mechanism of ACAT and allows  
CC the design of drugs serving as specific ACAT inhibitors, desirable  
CC for the prevention and/or treatment of human hypercholesterolaemia  
CC and human atherosclerosis. It also allows the design of antisense  
CC DNAs or RNAs to inhibit ACAT production, or probes to identify  
CC different forms of human ACAT or ACAT from different animal species.  
CC This sequence is a human ACAT cDNA clone designated C1.  
XX  
XX SQ Sequence 996 BP; 258 A; 219 C; 207 G; 312 T; 0 other;  
Query Match 8.6%; Score 134.6; DB 15; Length 996;  
Best Local Similarity 53.1%; Pred. No. 1.4e-23;  
Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;  
QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCTCTGTCATGAGCTGATGG 346  
DB 262 CACCTCCAGAAAGGAAGATTTTATTGCAAGGCGCTCTCTTAGATGAACCTGTG 321  
QY 347 AGGTGCAGCATTTCCGACCATCTACCAATGTTTCATCGCTGGCTGTGTCATCA 406  
DB 322 AAGTGACCATCATGACATATATACATGTTATTGCTCCCTCCTCATCTCTTTATCC 381  
QY 407 TCAGCACCTGGCCATCATGATGATGAGGCGCTGCTGCTG--AGTTTGACCT 464  
DB 382 TCAGCACACTTGTAGTATGATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 441  
QY 465 ACTG-ATCTTCAGCTTCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523  
DB 442 CCGTCTTATGCAATTTGGCAAAATTCCTACCGTTGTTGGACCTGGTGGATCATGTTCC 501  
QY 524 TCTCCACCTGTTGGCGCGCTACCAAGGCGCTACGCGCTGCGCGCGAGGCGACCTGGACGC 583

Db 502 TGTCTACATTTTCAGTTCCTATTTTCTGTTCAACATTTGGCGCACTGGCTATACAGA 561  
QY 584 AGCGACGGGCTGGGCTGTGCGCTTTTAGCGCCCGCCAGCCGCTGGTGCTC----- 633  
Db 562 GTTCTCATCCGCTGATCGTCTCTCTTCCATGGCTTTCTTTTCATGATCTTCCAGATTG 621  
QY 634 ---TGGCGCTCCCGGTCCACGTGGCGGTGGAGCATCAGCTCCCGCGGCTCCCGTTGT 690  
Db 622 GAGTTCTAGGTTTGGACCAACATATGTTGTAGCATATCTGCCACACGCTTCCCGG 681  
QY 691 GTCCCTGGCTTCGACGAGCTAGGTTCTCTGATGAAAAGCTACTCTCTCTCTGAGAGGCT 750  
Db 682 TTATCATTTATTCGACGAGCTGTTTGTATGAAGGCCACTCATTTGTCAGAGAGAC 741  
QY 751 GTCCCTGGGATCCTTCGTCGACAGAGGTGAGGGATCCAGGCC-----CCAGTTTCT 805  
Db 742 GTGCTCGGTACTATTTCAGCTAAGGAGAAATCAAGCACTGTTCATACCTACAGTCA 801  
QY 806 CGAGCTACCTTACTTCTCTCTGTCGCCCAACTCATCTACAGGAGACTTACCCTAGGA 865  
Db 802 ACAGTATTGTTACTTCTTATTGCTCTCTACCTTATCTACCGTGACAGCTATCCAGGA 861  
QY 866 CGCCCTATGTCAGGTGGAATTTATGTCGCAAGAACTTTGCCAGGCGCTGGGATGTGTC 925  
Db 862 ATCCCACTGTAAGATGGGTTATGTTGCTATGAAGTTTCACAGGCTTTTGGTGTCTTT 921  
QY 926 TCTATGCCCTGCTTCATCTCTGGGCGGCTCTGTGTTCTCTGTTGCAACATGAGCCGAG 985  
Db 922 TCTATGCTACTACATCTTTTGAAGGCTTTGTGCCCGCTTTGTCGGAATATCAACAGG 981  
QY 986 AGCCCTTCAGCACCC 1000  
Db 982 AGCCCTTCAGCGCTC 996

RESULT 13  
AAV01539  
ID AAV01539 standard; cDNA; 983 BP.  
XX AC AAV01539;  
XX DT 08-JUN-1998 (first entry)  
XX DE Human acylcoenzyme A:cholesterol acyltransferase II (ACAT II) DNA.  
XX KW Acylcoenzyme A:cholesterol acyltransferase; ACAT I;  
KW ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;  
KW inhibitor; atherosclerosis; hyperlipidaemia; human; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX FH Key Location/Qualifiers  
FT CDS 1..660  
FT /\*tag= a  
XX  
XX PN WO9745439-A1.  
XX PD 04-DEC-1997.  
XX PF 30-MAY-1997; 97WO-US09460.  
XX PR 30-MAY-1996; 96US-0657620.  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX Sturley SL;  
XX WPI; 1998-032573/03.  
XX P-PSDB; AAW43412.  
XX  
XX DNA encoding acylcoenzyme A: cholesterol acyltransferase II or  
PT III - useful to identify inhibitors for treatment of  
PT atherosclerosis or hyperlipidaemia







```

XX      This isolated nucleic acid molecule encodes human acylcoenzyme
CC      A:cholesterol acyltransferase II (see AAW43406), or ACAT related gene
CC      product 1 (ARGP-1), that is expressed at high levels in intestine
CC      and is a candidate for sterol esterification in these tissues. It
CC      was identified following database searching for human ACAT-related
CC      sequences and use of PCR and RACE to obtain full-length sequences.
CC      An isolated nucleic acid (see AAV01534) for human ARGP-2 (see AAW43407)
CC      was also identified. Also claimed are host vector systems for
CC      production of ARGP polypeptides, and transgenic non-human mammals.
CC      ARGP-1 and ARGP-2 nucleic acids can be used to diagnose or treat a
CC      subject who has an imbalance in sterol levels due to a defect in
CC      sterol esterification. A claimed oligonucleotide capable of
CC      specifically hybridising to a unique sequence of nucleotides in the
CC      isolated nucleic acid molecule, or a vector expressing the
CC      oligonucleotide, can be used to inhibit wild-type ARGP-1 or ARGP-2.
CC      The wild-type enzymes can be used to identify an inhibitor, useful
CC      in the treatment of atherosclerosis or hyperlipidaemia.
XX
SQ      Sequence 1521 BP; 277 A; 489 C; 412 G; 343 T; 0 other;

      Query Match          6.1%; Score 95; DB 19; Length 1521;
      Best Local Similarity 58.7%; Pred No. 1.2e-13;
      Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY      1019 TCCTGCATGCCACGTTGCCAGGATCTTCATGCTGCTCATCTCTTTTGCTTCTCTCC 1078
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      1079 ATTGCTGGCTCAACGCTTTGCCGAGATGCTAGGATTTGGAGACAGGATGTTCTACCGGG 1138
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      785 ACTCTGCTGCTGAATGCCGCTGGCTGAGCTCATGCGATTTGGAGACCGGGAGTTCTACCGGG 844
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      1139 ACTGTGGAACTCAAGCTCTTCTCCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      845 ACTGTGGAACTCCGAGTCTGTCACTTCTTGGCAGAACTGGAACTCCCTGTGCACA 904
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      1199 ACTGGCTGTACAGCTACGTTATCAGGATGGGCTCGGCTCTCTTGGTCCCGGGCCCGAG 1258
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      905 AGTGGTGCAATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGCAGCAGCAAGT 958
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      1259 GGGTAGCCATGCTGGGTGTGTTCTCGGCTCTCGGAGTGGCCCATGAGTATATCTTCTGCT 1318
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      959 GGATGCCAGGACAGGGGGTGTCTCTGGGCTCGGCTTTCTTCCACGAGTACCTGGTGAGCG 1018
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      1319 TCGTCTCTGGGGTTCTTC 1335
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
QY      1019 TCCCTCTGCGAATGTC 1035
DB      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |

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Search completed: April 30, 2003, 13:20:03  
Job time : 292 secs

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GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 13:13:06 ; Search time 53 Seconds  
(without alignments)  
9078.789 Million cell updates/sec

Title: US-09-918-026A-3  
Perfect score: 1569  
Sequence: 1 atggagcaggcgggccg.....cttggtctgcatactag 1569

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA.\*

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- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description       |
|------------|--------|-------------|--------|----|-------------------|
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| 2          | 405.6  | 25.9        | 4011   | 1  | US-08-121-057-3   |
| 3          | 405.6  | 25.9        | 4011   | 2  | US-08-509-187D-3  |
| 4          | 405.6  | 25.9        | 4011   | 2  | US-09-121-396-3   |
| 5          | 405.6  | 25.9        | 4011   | 5  | PCT-US93-09704A-3 |
| 6          | 359.8  | 22.9        | 4079   | 1  | US-08-121-057-2   |
| 7          | 359.8  | 22.9        | 4079   | 2  | US-08-509-187D-2  |
| 8          | 359.8  | 22.9        | 4079   | 2  | US-09-121-396-2   |
| 9          | 359.8  | 22.9        | 4079   | 5  | PCT-US93-09704A-2 |
| 10         | 134.6  | 8.6         | 996    | 1  | US-08-121-057-1   |
| 11         | 134.6  | 8.6         | 996    | 2  | US-08-509-187D-1  |
| 12         | 134.6  | 8.6         | 996    | 2  | US-09-121-396-1   |
| 13         | 134.6  | 8.6         | 996    | 5  | PCT-US93-09704A-1 |
| 14         | 95     | 6.1         | 1895   | 4  | US-09-326-203A-14 |
| 15         | 95     | 6.1         | 1976   | 3  | US-09-165-042-2   |
| 16         | 81.4   | 5.2         | 1650   | 4  | US-09-103-754A-2  |
| 17         | 79.8   | 5.1         | 1766   | 4  | US-09-326-203A-15 |
| 18         | 79.8   | 5.1         | 1766   | 4  | US-09-326-203A-16 |
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| 20         | 55.4   | 3.5         | 519    | 4  | US-09-326-203A-11 |
| 21         | 50     | 3.2         | 1942   | 4  | US-09-326-203A-1  |
| 22         | 42     | 2.7         | 3358   | 3  | US-09-248-571-2   |
| 23         | 42     | 2.7         | 3358   | 4  | US-09-553-736-2   |
| 24         | 41.2   | 2.6         | 7218   | 1  | US-08-232-463-14  |
| 25         | 40     | 2.5         | 629    | 4  | US-09-103-754A-3  |
| 26         | 39.8   | 2.5         | 2970   | 4  | US-09-110-517-3   |
| 27         | 39.8   | 2.5         | 5173   | 1  | US-08-242-677-1   |

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|----|------|-----|-------|---|-------------------|--------------------|
| 28 | 39.4 | 2.5 | 20235 | 1 | US-07-642-734C-3  | Sequence 3, Appli  |
| 29 | 39.4 | 2.5 | 20235 | 3 | US-08-439-009A-3  | Sequence 3, Appli  |
| 30 | 39.2 | 2.5 | 1469  | 5 | PCT-US92-08258-1  | Sequence 1, Appli  |
| 31 | 39.2 | 2.5 | 2353  | 5 | PCT-US92-06840-1  | Sequence 1, Appli  |
| 32 | 39   | 2.5 | 289   | 4 | US-09-007-005-17  | Sequence 17, Appli |
| 33 | 39   | 2.5 | 289   | 4 | US-09-244-796-17  | Sequence 17, Appli |
| 34 | 39   | 2.5 | 2474  | 2 | US-08-666-392A-2  | Sequence 2, Appli  |
| 35 | 39   | 2.5 | 2474  | 4 | US-09-199-926-2   | Sequence 2, Appli  |
| 36 | 39   | 2.5 | 33529 | 1 | US-09-144-085-3   | Sequence 3, Appli  |
| 37 | 38.8 | 2.5 | 30001 | 1 | US-08-125-468-1   | Sequence 1, Appli  |
| 38 | 38.8 | 2.5 | 30001 | 2 | US-08-474-933-1   | Sequence 1, Appli  |
| 39 | 38.6 | 2.5 | 2080  | 2 | US-08-878-563A-2  | Sequence 2, Appli  |
| 40 | 38.6 | 2.5 | 2080  | 4 | US-09-270-117-2   | Sequence 2, Appli  |
| 41 | 38.6 | 2.5 | 2430  | 4 | US-09-105-537-23  | Sequence 23, Appli |
| 42 | 38.6 | 2.5 | 13613 | 4 | US-09-105-537-3   | Sequence 3, Appli  |
| 43 | 38.4 | 2.4 | 500   | 3 | US-09-141-000-2   | Sequence 2, Appli  |
| 44 | 38.4 | 2.4 | 696   | 4 | US-09-461-697-193 | Sequence 193, App  |
| 45 | 38.4 | 2.4 | 696   | 4 | US-09-461-697-191 | Sequence 191, App  |

ALIGNMENTS

RESULT 1  
US-09-165-042-4  
; Sequence 4, Application US/09165042  
; Patent No. 6100077  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.  
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL  
; FILE REFERENCE: ACYLTRANSFERASE  
; FILE REFERENCE: 0575/56331  
; CURRENT APPLICATION NUMBER: US/09/165,042  
; CURRENT FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Yeast  
US-09-165-042-4

|                       |              |   |               |              |
|-----------------------|--------------|---|---------------|--------------|
| Query Match           | 99.7%        | Score 1564.2;   | DB 3;         | Length 2040; |
| Best Local Similarity | 99.8%        | Pred. No. 0;  |               |              |
| Matches 1566;         | Conservative | 0;  | Mismatches 3; | Indels 0;    |
| Gaps                  | 0;           |   |               |              |
| Qy                    | 1            | ATGGAGCCAGGCGGGCGCGTCTGCTGTCAGAGACAGAGAGGCTGGAGGGGAGCGG     | 60            |              |
| Db                    | 52           | ATGGAGCCAGGCGGGCGCGTCTGCTGTCAGAGACAGAGAGGCTGGAGGGGAGCGG     | 111           |              |
| Qy                    | 61           | GAGCGCCACCTGTGGAGATGGAACACTGAGACGACAGAGCCCGGACTTGGTACAA     | 120           |              |
| Db                    | 112          | GAGCGCCACCTGTGGAGATGGAACACTGAGACGACAGAGCCCGGACTTGGTACAA     | 171           |              |
| Qy                    | 121          | TGGACCCGACACATGAGGCTGTGAAGGCACAAATTCCTGGAGCAAGCGGAGGACAATG  | 180           |              |
| Db                    | 172          | TGGACCCGACACATGAGGCTGTGAAGGCACAAATTCCTGGAGCAAGCGGAGGACAATG  | 231           |              |
| Qy                    | 181          | AGGAGACTGCTGGATCGGGCCCATGCGGGAGGCTATACAATCTTACCATCACAAGACAA | 240           |              |
| Db                    | 232          | AGGAGACTGCTGGATCGGGCCCATGCGGGAGGCTATACAATCTTACCATCACAAGACAA | 291           |              |
| Qy                    | 241          | CTCTCTGCCCCACCTCCCGGCTTCTTGGAGCAGGACCCAGGAGCCCTCCCTGGGGAA   | 300           |              |
| Db                    | 292          | CTCTCTGCCCCACCTCCCGGCTTCTTGGAGCAGGACCCAGGAGCCCTCCCTGGGGAA   | 351           |              |
| Qy                    | 301          | CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTATGAGCTGATGAGGTGCAGCATTTTC | 360           |              |
| Db                    | 352          | CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTATGAGCTGATGAGGTGCAGCATTTTC | 411           |              |
| Qy                    | 361          | CGACCATCTACACATGTTTCATGCTGCGCTGTGTCTTTCATCATCAGCACCCCTGGCC  | 420           |              |

Db 412 CGCACCCTACACATGTTTCATCGCTGGCTGTGTCTTTCATCATCAGCACCTGGCC 471  
QY 421 ATGACTTTCATGATGAGGCAAGCTGTGCTGGAGATTGACCTACTGATCTTCAGCTTC 480  
Db 472 ATGACTTTCATGATGAGGCAAGCTGTGCTGGAGATTGACCTACTGATCTTCAGCTTC 531  
QY 481 GGACAGCTGCATGCGCTGTGAGCTGGGTGCCATGTTCTGTCCACCTGTGGCG 540  
Db 532 GGACAGCTGCATGCGCTGTGAGCTGGGTGCCATGTTCTGTCCACCTGTGGCG 591  
QY 541 CCGTACAGCCCTACGGCTGTGGGCAAGGCACTGTGACGAGCGAGCGGCTGGGC 600  
Db 592 CCGTACAGCCCTACGGCTGTGGGCAAGGCACTGTGACGAGCGAGCGGCTGGGC 651  
QY 601 TGTGCGCTTTAGCGGCCAGCGCTGTGCTGTGCGCGCTGCCGTGACAGTGGCGCTG 660  
Db 652 TGTGCGCTGTAGCGGCCAGCGCTGTGCTGTGCGCGCTGCCGTGACAGTGGCGCTG 711  
QY 661 GAGCATCAGCTCCCGCGGCTCCCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 720  
Db 712 GAGCATCAGCTCCCGCGGCTCCCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 771  
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QY 781 GAGGGATCCAGGCCCCAGTTTCTCCAGCTACCTTCTTCTTCTTCTTCTTCTTCTTCT 840  
Db 832 GAGGGATCCAGGCCCCAGTTTCTCCAGCTACCTTCTTCTTCTTCTTCTTCTTCTTCT 891  
QY 841 ATCTACAGGAGACTTACCCTAGGACCCCTATGTCAGGTGGATATGTTGGCCAGAAC 900  
Db 892 ATCTACAGGAGACTTACCCTAGGACCCCTATGTCAGGTGGATATGTTGGCCAGAAC 951  
QY 901 TTTGCCAGGCTTGGATGTGCTGTATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTT 960  
Db 952 TTTGCCAGGCTTGGATGTGCTGTATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTT 1011  
QY 961 CTGTCTTTGCAACATGAGCGAGAGCCCTTACAGACCCGCTGCTGCTGCTGCTATC 1020  
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QY 1021 CTGATGCCAGTGTGCGAGGATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 1080  
Db 1072 CTGATGCCAGTGTGCGAGGATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 1131  
QY 1081 TGCTGGCTCAACGCTTTGCGAGATGCTAGCATTTGGAGACAGGATGTTCTACCGGAC 1140  
Db 1132 TGCTGGCTCAACGCTTTGCGAGATGCTAGCATTTGGAGACAGGATGTTCTACCGGAC 1191  
QY 1141 TGGTGGAACTCAACGCTTCTTCCAACTACTACCGCACTTGAACGTTGGTGGTCCATGAC 1200  
Db 1192 TGGTGGAACTCAACGCTTCTTCCAACTACTACCGCACTTGAACGTTGGTGGTCCATGAC 1251  
QY 1201 TGGCTGTACAGCTACGTATCAGATGGGTGGGCTGCTTGGTGGCCGCGCGAGGG 1260  
Db 1252 TGGCTGTACAGCTACGTATCAGATGGGTGGGCTGCTTGGTGGCCGCGCGAGGG 1311  
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Db 1312 GTAGCCATGCTGGGTGTGCTGCTGCTCCGAGTGGGCCATGATATATCTTCTGCTTC 1371  
QY 1321 GTCTGGGGTCTTCTATCCCGTCAAGTGTATCTTCTTCTTCTTCTTCTTCTTCTTCT 1380  
Db 1372 GTCTGGGGTCTTCTATCCCGTCAAGTGTATCTTCTTCTTCTTCTTCTTCTTCTTCT 1431  
QY 1381 AACTTCATGATCATGACAGCGACCGCGGATGAGGCTGCTGATGTGGAGCAATG 1440  
Db 1432 AACTTCATGATCATGACAGCGACCGCGGATGAGGCTGCTGATGTGGAGCAATG 1491  
QY 1441 CTGTTTCTAGGCGAGGGAATCCAGGTGACGCTGTACTGCCAGGAGTGTACGACGGCG 1500  
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QY 1501 CACTGCCCTTACCCAGGCAACTTCTGGGGCTGTGTGACACCTCGATCTTGGTCTGC 1560  
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QY 1561 CATACCTAG 1569  
Db 1612 CATACCTAG 1620

RESULT 2  
US-08-121-057-3  
; Sequence 3, Application US/08121057  
; Patent No. 5484727  
; GENERAL INFORMATION:  
; APPLICANT: CHANG, TA-YUAN  
; APPLICANT: CHANG, CATHERINE C. Y.  
; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL  
; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MA USA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,057  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LAMPORT HAMMITTE, ANN.  
; REGISTRATION NUMBER: 34,858  
; REFERENCE/DOCKET NUMBER: DCI-033CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-2700  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4011 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1397..3046  
; US-08-121-057-3

Query Match 25.9%; Score 405.6; DB 1; Length 4011;  
Best Local Similarity 58.9%; Pred. No. 1.1e-94;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

QY 287 CATCCCTGGGAAACAGAAAGTTTTCATATCCCAAGTCCCTGCTGTGATGAGCTGATGG 346  
Db 1737 CACCTCCAGAACAGAAAGATTTTATTCAGAGCGCTCTCTCTTAGATGAATGCTGTG 1796  
QY 347 AGGTGGAGCATTTCCGACCATCTACCATGTTTCATCGTGGCTGTGTCTTTCATCA 406  
Db 1797 AAGTGGAGCATTCAGAACATATATCATGTTTATTCGCTCTCTCTCTCTTTATCC 1856  
QY 407 TCAGCACCTCGGCCATCGACTTCATTTGATGAGGCGAGGCTGCTGCTGAGTTGACCTAC 466  
Db 1857 TCAGCACCTGTAGTAGATTACATTTGATGAGGAGGCTGGTCTGTTGAGTTACGCTCC 1916  
QY 467 TGATCTTCAGCTTCGGACAGCTGCCATGGCGCTGGTGGTACCTGGGTCCTGTTCTGT 526



Db 2037 CTCATCGCTGATCCGTTCTCTCTCCATGGCTTCTTTTCATGATCTTCCAGATTGGAG 2096  
QY 647 TCC-----ACGTGCGCTGGAGATCAGCTCCCGCGCGCTCCCGTT 688  
Db 2097 TTTAGTGTGGACCAACATATGTTGTAGCATATACATGCCACGCTCCCGGT 2156  
QY 689 GTGTCCTGGTCTTGGACGAGTTAGTTCCTGATGAAAGCTACTCTTCTTCCAGAGAGG 748  
Db 2157 TCATCATATATTCGACGAGATCGTTTGTAAAGAGGCCACTCATTTGTTCAGAGAGA 2216  
QY 749 CTGTGCTGGATCTTCTGTCGACAGAGGTGAGGGATCCAGGCCCGCCAGTTTCTCCA 808  
Db 2217 ACGTGCGCTGGGTACTAAAT--TCAGTAAAGAGAAATCAAGCACTGTTCCTCAATACCTACA 2275  
QY 809 G-----CTACCTCTACTTCTCTTCTGCCCCAACACTCATCTACAGGAGACTTACCCCT 861  
Db 2276 GTCAACCAATTTGTACTCTTATTTGCTCCTACCCTTATACCGTGACAGCTATCCC 2335  
QY 862 AGGACGCCCTATGTGAGTGGAAATATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATGT 921  
Db 2336 AGGAATCCACTGTAAAGATGGGTATGTGCTATGAAGTTTGCACAGGCTTTGGTTGC 2395  
QY 922 GTGCTCTATGCTGCTTCACTCTGCGCGCTCTGTCTCTGCTTCTGCTTTCGCAATGAGC 981  
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QY 982 CGAGAGCCCTTTCAGCACCGCTGCTGTCTCTATCTCTGATGCGAGTTCGCCAGGC 1041  
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QY 1042 ATCTTTCATGCTGCTCATCTCTTTCCTTCCCTTCTCTCACTGCTGCTCAAGCCCTTTGCC 1101  
Db 2516 GTGCTGATCTCTCTCTTACTTCTTCTTCTTCTTCTGCACTGCTGCTCAATGCTTGTCT 2575  
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QY 1342 GTCATGCTGATCTCTTCTGCTCATTTGGAGGAATGTTGAATTCATGATGATGATAGT 1401  
Db 2816 GTGCTGTTGCTGCTCTTCTATGTTCTTGGAAATGGCTTTTCAACTTCATTTCAATGATAGT 2875  
QY 1402 CGCACGGCGCGCATGGAACCTGCTGATGTGACCATGCTTTTCTAGGCCAGGGAATC 1461  
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QY 1462 CAGGTGAGCTGCTTACTGCGAGAGTGGTACGACGCGGCACTGCCCTTACCCACGGA 1521  
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QY 1522 ACTTCTGGGGGTGTTGACACTCGATCTTGGTCTGCCAT 1563  
Db 2996 ACATTTTGGATTTATGTCGGGCGACGTTCTCTGGACTGTGCTG 3037

RESULT 4  
US-09-121-396-3  
; Sequence 3, Application US/09121396  
; Patent No. 5968749  
; GENERAL INFORMATION:

APPLICANT: CHANG, TA-YUAN  
APPLICANT: CHANG, CATHERINE C. Y.  
TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL  
TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHIVE & COCKFIELD  
STREET: 28 STATE STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,396  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/509,187  
FILING DATE: 07/31/95  
ATTORNEY/AGENT INFORMATION:  
NAME: LAMPORT HAMMITTE, ANN.  
REGISTRATION NUMBER: 34,858  
REFERENCE/DOCKET NUMBER: DCI-033CPDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-2700  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4011 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-09-121-396-3

Query Match 25.9%; Score 405.6; DB 2; Length 4011;  
Best Local Similarity 58.9%; Pred. No. 1.le-94;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;  
QY 287 CATCCCTGGGAAACAGAAAGTTTTCATATCCGCAAGTCCCTGCTGTGATGAGCTGATG 346  
Db 1737 CACCTCCAGAACAGAAAGATTTTATTGCAAGGCGCTCTCTTAGATGAAGCTGTG 1796  
QY 347 AGGTGACAGATTTCCGACCATCTACCATATGTTTACATGCTGCGCTGCTGTGCTTCATCA 406  
Db 1797 AAGTGGACCATCAGAACAAATATATCATGTTTATTGGCCCTCCTCATCTCTTTATCC 1856  
QY 407 TCACACCCCTGGCCATCGACTTCATTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTAC 466  
Db 1857 TCAGACACACTGTGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1916  
QY 467 TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGAACCTGGGTCGCCATGTTCTGT 526  
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QY 527 CCACCTGTTGGCGCGGTACAGGCCCTACGGCTGTGGCCAGGGGACACCTGGAGCAGG 586  
Db 1977 CTACATTTTCAAGTTTCCCTATTTTCTGTTTCAACATTTGGCCACCTGCGCTATGCAAGAGTT 2036  
QY 587 CGACGGGCTGGGCTGTGCGCTTTTAGCGCCACGCGCGCTGCTGCTGCGCTGCGCGG 646  
Db 2037 CTCATCCCTGATCCGTTCTCTCTTCCATGCTTCTTTTCATGATCTTCCAGATTGGAG 2096  
QY 647 TCC-----ACGTGCGCGCTGGAGCAATCAGCTCCCGCGCGCTCCCGTT 688  
Db 2097 TTCTAGGTTTTGGACCAACATATGTTGTTAGCATATACACTGCGCACCACTTCCCGGT 2156  
QY 689 GTGTCTGCTCTTTCAGCAGGTTAGTTCTTCCATGATGATGATGATGATGATGATGATG 748







[illegible]

## RESULT 7

```

US-08-509-187D-2
; Sequence 2, Application US/08509187D
; Patent No. 5834283
;
; GENERAL INFORMATION:
;
; APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.
;
; TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase
;
; NUMBER OF SEQUENCES: 9
;
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/509,187D
; FILING DATE: 31-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lampert Hammitte, Ann
; REGISTRATION NUMBER: 34,858
; REFERENCE/DOCKET NUMBER: DCI-033cpdv
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
; US-08-509-187D-2

```

| Query Match           | 22.9%;          | Score 359.8;  | DB 2;      | Length 4079; |
|-----------------------|-----------------|---|------------|--------------|
| Best Local Similarity | 58.0%;          | Pred. No. 6.6e-83;  |            |              |
| Matches 722;          | Conservative 0; | Mismatches 502;   | Indels 21; | Gaps         |
| QY                    | 287             | CATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAGTCCTCGCTTCATCAGCTGATGG   | 346        |              |
| DB                    | 1808            | CACCTCAGAACAGGAAGATTTTATTTGCAAGCGCTCTCTTTAGATGACATGCTTG       | 1867       |              |
| QY                    | 347             | AGGTGAGCATTTTCGCACCATCTACCAACATTTTCATCGCTGGCCTGTGCTCTCATCA    | 406        |              |
| DB                    | 1868            | AAGTGACCACATCAGAACAAATATACATGTTTATTGGCCTCCTCTCTTTATTC         | 1927       |              |
| QY                    | 407             | TCAGCACCTTGGCCATCGACTTCATTGATGAGGGCAGGCTGCTGCTGG--AGTTTGACCT  | 464        |              |
| DB                    | 1928            | TCAGCACACTGTAGTAGATATACATGTATGAAGGAAGCTGGTGTCTGCAAGTTTACCGCT  | 1987       |              |
| QY                    | 465             | ACTG-ATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGTGACCTGGGTGGCCATGTTTC  | 523        |              |
| DB                    | 1988            | CTGTCTTATGCATTTTGGCAAAATTTCTTACCCTTGTGTGGACCTGGTGATCATGTTCC   | 2047       |              |
| QY                    | 524             | TGTCCACCCCTGTGGCCGCTACCAAGGCCCTACGGCTGTGGGCCAAGGGCACCTTGGACGC | 583        |              |
| DB                    | 2048            | TGTCTACATTTTCAGTTCCCTATTTTCTGTTTCAACATTTGGCGCACTGGCTATAGCAAGA | 2107       |              |
| QY                    | 584             | AGGGAGGGCCTGGGCTGTGGCTTTTAGCGCCGCCAGCCGTGGTGTCTTCGCGGCTGC     | 643        |              |
| DB                    | 2108            | GTTCTCATCCGCTGATCCGCTTCTCTCTCCATTGGCTTTCTTTTCATGATCTTCCAGATTG | 2167       |              |
| QY                    | 644             | CGTCCAGTGGCG-----TGGAGCATCAGCTCCCGCGGCTCCCGTTGT               | 690        |              |
| DB                    | 2168            | GAGTCTTAGTPTTGGACCAACATATGTTGTGTTTAGCATATCTTGGCCACCAGCTTCCCGG | 2227       |              |
| QY                    | 691             | GTCTGTGCTTTCGAGCAGGTTAGTGTCTTGATGAAAGCTACTCTCTCTCGCAGAGGCT    | 750        |              |
| DB                    | 2228            | TTTCATCATTATTCGACAGATCGTTTGTGTAAGAGCCCACTCATTTGTGACAGAGAAC    | 2287       |              |
| QY                    | 751             | GTGCTGGGATCCTTCGTGCCAGAGAGTGAAGGGATCCAGGCG-----CCCAGTTTCT     | 805        |              |
| DB                    | 2288            | GTGCTCGGCTACTAATTCAGCTAAGAGGAAATCAAGCACTGTTCCAAATACCTACAGTCA  | 2347       |              |
| QY                    | 806             | CCAGCTACCTCTACTTCTCTTCTGCCCAACACTCATCTACAGGAGACTTTACCTTAGGA   | 865        |              |
| DB                    | 2348            | ACCAGTATTTGTACTTCTTATTTGTCTCTTACCTTATCTACCGTGACAGCTATCCCCAGA  | 2407       |              |
| QY                    | 866             | CGCCCTATGTACGGTGGAAATATGTGGCCCAAGAACTTTGCCACGCCCTGGGATGTGTGC  | 925        |              |
| DB                    | 2408            | ATCCCACTGTAAAGTGGGTTATGTGCTATCAAGTTTTCACAGGCTCTTGGTGTCTTT     | 2467       |              |
| QY                    | 926             | TCTATGCTGCTTTCATCTCTGGGCGGCTCTGTGTTCTCTGTTTGGCCAAATGACCGCAG   | 985        |              |
| DB                    | 2468            | TCTATGTGACTACACTTTTGAAGGCTTTGTGCCCTTTGTTCGGAATATCAAAACAGG     | 2527       |              |
| QY                    | 986             | AGCCCTTCAGCACCCGTGCGCTCTCTATCTTCATGCCACAGTTCGCCAGGCATCT       | 1045       |              |
| DB                    | 2528            | AGCCCTTCAGCGCTCGTGTCTGTGGTCTATGTGTAATTTAACTTCCATCTTGGCAGGTGTC | 2587       |              |
| QY                    | 1046            | TCATGCTGCTGTCTACTTCTTTTGGCTTCTCTCATTTGGCTCAAGCCCTTTGCCGAGA    | 1105       |              |
| DB                    | 2588            | TGATTCTCTCTTACTTTTTTTTTGGCTTTTTCGACTGTGCTCAATGCCCTTGTCTGAGA   | 2647       |              |
| QY                    | 1106            | TGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGCTCTCTCCA   | 1165       |              |
| DB                    | 2648            | TGTTACGCTTTTGTGACAGGATGTTCTATAAGGATTTGGTGGAACTCCACGCTACATCCA  | 2707       |              |
| QY                    | 1166            | ACTTACTACCGCATTTGGAAGTGTGGTCCATGACTGGGTGTACAGCTACGTGTATCAGG   | 1225       |              |
| DB                    | 2708            | ACTATTATAGAACTTGGGATGTGGTGCATGACTGGCTATATTACTATGCTTACAAGG     | 2767       |              |
| QY                    | 1226            | ATGGGCTCGGGCTCTTGTGTCGCCGGCCGAGGGTAGCCATGCTGGGTGTTCTCTCG      | 1285       |              |
| DB                    | 2768            | ACTTCTCTGTTTTTCTCCAAGAGATTCAAATCTGCTGCCATGTTAGCTGTCTTTGCTGT   | 2827       |              |
| QY                    | 1286            | TCGCCGAGTGGCCCATGAGTATATCTTCTGCTCTCGCTCGGGTCTTCTTATCCCCGTCA   | 1345       |              |

US-08-509-187D-2

|    |      |   |      |
|----|------|---|------|
| Db | 2828 | TATCTGCTGTAGTACACGAATATGCCCTTGCTTGCCTTTCCTATCCCGTCG             | 2887 |
| QY | 1346 | TGCTGATACTCTCTCTCATTTGGAGGAATGTTGAACTTCATGATGCATGACACCGCA       | 1405 |
| Db | 2888 | TGTTGCTGCTCTTCATGTTCTTTTGGAAATGGCTTTTCAACTTCATGTGTAATGATAGTCGGA | 2947 |
| QY | 1406 | CCGGCCCCGGCATGGAACCTGCTGATGTGGACCATGCTTGTTCATAGGCCAGGGAAATCCAGG | 1465 |
| Db | 2948 | AAAAGCCGATTTGGAAATGTTCTGATGTGGACTTCTCTTTCTTGGGCAATGGAGTCTTAC    | 3007 |
| QY | 1466 | TCAGCCTCTACTGCCAGAGTGGTAGCAGCGGGCGACTGCCCTT                     | 1510 |
| Db | 3008 | TCCTGCTTTTATCTCAAGAAATGGTATGCACGCTCGGCCTGCTAGCT                 | 3052 |

## RESULT 8

US-09-121-396-2  
 ; Sequence 2, Application US/09121396  
 ; Patent No. 5968749  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHANG, TA-YUAN  
 ; APPLICANT: CHANG, CATHERINE C. Y.  
 ; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL.  
 ; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 28 STATE STREET  
 ; CITY: BOSTON  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII Text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/121,396  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/509,187  
 ; FILING DATE: 07/31/95  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: LAMPORT HAMMITTE, ANN.  
 ; REGISTRATION NUMBER: 34,858  
 ; REFERENCE/DOCKET NUMBER: DCI-033CPDV  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-2700  
 ; TELEFAX: (617) 742-4214  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; -SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4079 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-09-121-396-2

|    |      |  |      |
|----|------|--|------|
| Qy | 407  | TCAGCACCTGGCCATCGACTTCATTGATGAGGCAGGCTGCTGCTGG--AGTTTGACCT     | 464  |
| Db | 1928 | TCAGCACACTTAGTAGTATACATTGATGAAGGAAGGCTGGTGCTTGCAGTTACGCCT      | 1987 |
| Qy | 465  | ACTG-ATCTTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGAOCTGGGTGCCATGTTTC   | 523  |
| Db | 1988 | CTGTCTTATGCATTTTGGCAAATTTCCCTACCGTTGTTGGACCTGGTGGATCATGTTCC    | 2047 |
| Qy | 524  | TGTCCACCTGTTGGGCGGTACACAGGCCCTACGGCTGTGGGCCAGGGCACCTCGACGC     | 583  |
| Db | 2048 | TGTCTACATTTTTCAGTTCCCTATTTTCTGTTTCAACATATTGGCGCATGGCTATAGCAAGA | 2107 |
| Qy | 584  | AGCGACGGGCTTGGCGTGTGGCGTTTTAGCGGCCACGCGTGGTCTCTCGCGCTGC        | 643  |
| Db | 2108 | GTTCCTCATCGCTGATCCGTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTG     | 2167 |
| Qy | 644  | CGGTCCACGTGCCG-----TGGAGCATCAGTCCGCGCGGCTCCCCGTTGT             | 690  |
| Db | 2168 | GAGTTCTAGTTTTGGACCAACATATGTTGTGTAGCATCTGCCACACAGTCTCCCG        | 2227 |
| Qy | 691  | GTCTGTGTTTCGACGAGTTAGTTCTCTGATGAAGAGCTACTCTTCCTGACAGAGGCT      | 750  |
| Db | 2228 | TTCATCATATTTCGACGAGATCGTTTGTGTAATGAAGGCCCACTCATTTGTTCAGAGAGAAC | 2287 |
| Qy | 751  | GTGCCTGGGATCCTTCGTGCCACGAGGTGAGGGATPCCAGGC-----CCAGTTTCT       | 805  |
| Db | 2288 | GTSCCTGGGTACTAATTTCAGCTAAGAGAAATCAAGCACTGTTTCCAAATACCTACAGTCA  | 2347 |
| Qy | 806  | CGAGCTACCTCTACTTCTCTTCTGCCAAACACATCATCAGAGGAGACATTACCTTAGGA    | 865  |
| Db | 2348 | ACCAGTATTGTACTTCTTATTGTCTCTACCTTATCTACCGTGACAGCTATCCACGGA      | 2407 |
| Qy | 866  | CGCCCTATGTCAAGTGAATATTATGTGCCAAGAACTTTGCCAGGCCCTGGGATGTGTC     | 925  |
| Db | 2408 | ATCCACTGTAAAGATGGGTTATGTTGTATGAAGTTTGCACAGGCTTTTGGTTGCTTTT     | 2467 |
| Qy | 926  | TCATGCTGCTTCATCCTTGGCGGCTCTGTGTCTCTTTCGCAACATGAGCGGAG          | 985  |
| Db | 2468 | TCATGTGTACTACATCTTTGAAGGCTTTGTGCCCCCTGTTTCGGAATATCAACAGG       | 2527 |
| Qy | 986  | AGCCCTTCAGACCCGTGCCCTGGTGCTCTCTATCCTGCATGCCAGTTCGCCAGGCATCT    | 1045 |
| Db | 2528 | AGCCCTTCAGCGCTGTTCTGCTGCTATGTTAACTCCATCTTGCACAGTGTGC           | 2587 |
| Qy | 1046 | TCATGCTGCTGCATCTTCTTTTGGCTTCCCTCCATGCTGCTCAACGCCCTTGGCCGAGA    | 1105 |
| Db | 2588 | TGATTCTCTTCTTACTTTTTTTTGGCTTTTTCACACTGCTGCTCAATGCCCTTGTCTGAGA  | 2647 |
| Qy | 1106 | TGCTACGATTTGGAGACAGATGTTCTACGGGACTGTGGAACCTCAACGTCCTTCTCCA     | 1165 |
| Db | 2648 | TGTTACGCTTTGGTGACAGGATGTTCTATAGAGATTGGTGAACCTCCAGTCTACTCCA     | 2707 |
| Qy | 1166 | ACTACTACCCACTTGGACGTGGTGGTCCATGACTGGCTGTACAGCTPAGCTGATCAGG     | 1225 |
| Db | 2708 | ACTATTATAGAACTGSAATGTGGTGCTCATGCTGGCTATATTACTATGCTTTACAAGG     | 2767 |
| Qy | 1226 | ATGGGCTGGGCTCTTGTGTCGCCGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTCGG      | 1285 |
| Db | 2768 | ACTTTCCTGGTTTTCTCCAGAGATTCAAATCTGCTGCCATGTAGCTGTCTTTGCTG       | 2827 |
| Qy | 1286 | TCTCCGAGTGGGCCATGAGTATATCTTCTGCTCTGCTCTGGGTTCTTCTATCCCGTCA     | 1345 |
| Db | 2828 | TATCTGTGTAGTACAGGAATATGCCCTTGGCTGTTTGTGAGCTTTTCTATCCCGTGC      | 2887 |
| Qy | 1346 | TGCTGATCTCTTCTCTTGTTCATTGGAGGAATGTTGAACATTGATGATGATGACCGGCA    | 1405 |
| Db | 2888 | TGTTCTGCTCTTCATCTTCTTTTGGAAATGGCTTTTCAACTTTCATGTCATATAGTCGGA   | 2947 |
| Qy | 1406 | CGGCGCCGGCATGGAAGCTGCTCATCTGACCATGCTGTTCTTAGGCCACGGAATCCAGG    | 1465 |
| Db | 2948 | AAAAGCCGATTTGGAATGTTCTCATGTGGACTTCTCTTTCTTGGGCAATGGAGTCTTAC    | 3007 |
| Qy | 1466 | TCAGCCTGTACTGCCAGGAGTGTAGCAGCGGCACTGCCCTT                      | 1520 |

Db 3008 TCTGCTTTTATCTCAAGAAATGGTATGCACGTCGGCACTGTACCT 3052

RESULT 9

PCT-US93-09704A-2

; Sequence 2, Application PC/TUS9309704A

; GENERAL INFORMATION:

; APPLICANT: ACYL COENZYME A: CHOLESTEROL

; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

; NUMBER OF SEQUENCES: 9

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/09704A

; FILING DATE: October 12, 1993

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. SER. NO. 959,950

; FILING DATE: October 14, 1992

; APPLICATION NUMBER: U.S. SER. NO. 121,057

; FILING DATE: September 10, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: LAMPORT HAMMITTE, ANN.

; REGISTRATION NUMBER: 34,858

; REFERENCE/DOCKET NUMBER: DCI-033CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-2700

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4079 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; PCT-US93-09704A-2

Query Match 22.9%; Score 359.8; DB 5; Length 4079;

Best Local Similarity 58.0%; Pred. No. 6.6e-83;

Matches 722; Conservative 0; Mismatches 502; Indels 21; Gaps 4;

QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTATGAGCTGATGG 346  
 Db 1808 CACCTCCAGAACAGAAAGATTTTATTTGCAAGCGCTCTCTTAGATGAACCTGCTTG 1867  
 QY 347 AGGTGCAGCATTTCCGCGCACCATCTACCACATGTTTCATCGCTGGCCTGTGTCTTCATCA 406  
 Db 1868 AAGTGGACACATCAGAACATATATCATGTTTATTTGCCCTCCTCATCTCTTTATCC 1927  
 QY 407 TCAGCACCTGGCCATCGACTTCATGATGAGGGCAGGCTGCTGTGG--AGTTGACCT 464  
 Db 1928 TCAGCACACTTGTAGTAGATTACATTGATGAAGGAAGGCTGTGCTTGAAGTACGCT 1987  
 QY 465 ACTG-ATCTTACGTTCCGACAGCTGCCATTGGCGCTGTGTACCTGGGTGCCCATGTTTC 523  
 Db 1988 CTTGCTTTATGATTTTGGCAAATTTCTTACCGTTGTTTGGACCTGGTGGATCATGTGTC 2047  
 QY 524 TGTCCACCTGTTGGCGCGCTACACGCGCTACGCGCTGTGGCCAGGGGCACTGGACGC 583  
 Db 2048 TGTCTACATTTTCAGTTCCTATTTTCGTTTCAACATTTGGCGCACTGGCTATACGA 2107  
 QY 584 AGGCGACGGCTGGGCTGTGGCTTTTAGCGCCACGCGCTGTGTGCTGCGCGCTGC 643  
 Db 2108 GTTCTCATCCGCTGATCCCTTCTCTCTCATGCGCTTTCTTTTCATGATCTTCCAGATG 2167  
 QY 644 CGGTCCACGTGGCG-----TGGAGCATCAGTCCCGCGCTCCCGTGT 690  
 Db 2168 GAGTTCTAGTTTGGACCAACATATGTTGTAGCATATCTGCCACCACTTCCCGG 2227

QY 691 GTCCCTGGTCTTCGAGCAGGTTAGGTTTCTGATGAAAAAGTACTCTCTCTCTGAGAGGCT 750  
 Db 2228 TTCATCATATTTCGAGCAGATCGTTTGTATGAGGCCACTCATTTGTGAGAGAGA 2287  
 QY 751 GTGCTGGGATCCTTCGTCGACAGAGGTGAGGGATGCCAGGCC-----CCAGTTTCT 805  
 Db 2288 GTGCTCGGGTACTAATTCAGCTAAGAGAAATCAAGCACTGTTCCAAATACATACAGTCA 2347  
 QY 806 CCAGTACCTCTACCTCTCTCTGCCCCAACACTCATACAGGGAGACTTACCCATAGCA 865  
 Db 2348 ACCAGTATTGTACTTCTTATTTGCTCTACCTTATCTACCGTGACAGCTATCCAGGA 2407  
 QY 866 GCCCTATGTCAGGTGGAATTTATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATGTGTC 925  
 Db 2408 ATCCCACTGTAAGATGGGTTATGTGCTATGAAGTTTGCACAGGCTTGTGTTGCTTTT 2467  
 QY 926 TCTATGCTGCTTCATCTGCGGCCCTCTGTGTCCTGTCCTTTGCCAACATGAGCCGAG 985  
 Db 2468 TCTATGCTGCTTACATCTTTGAAAGGCTTTGTGCCCTTGTTCGGAATATCAACAGG 2527  
 QY 986 AGCCCTTCAGCACCGCTGCCCTGGTCTCTCTCTGCTGATGCTGCTGCTGCTGCTGCT 1045  
 Db 2528 AGCCCTTCAGCGCTGCTGTTCTGCTGCTTAACTCCATCTTTCAGGCTGTCG 2587  
 QY 1046 TCATGCTGCTGCTCATCTTTTGTGCTTCTCCATTTGCTGCTCAACGCTTTTGCAGGAGA 1105  
 Db 2588 TGATTCTCTCTTACTTTTGTGCTTTCGCACTGCTGCTCAATGCTTGTGCTGAGA 2647  
 QY 1106 TGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGTTGGAACCTCAACGCTTCTTCCA 1165  
 Db 2648 TGTACGCTTTGGTGCACAGGATGTTCTATAAGGATTTGTTGGAACCTCCAGTCTATCCA 2707  
 QY 1166 ACTACTACCGCACTTGGAGAGGTTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225  
 Db 2708 ACTATTAGAACCTGGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2767  
 QY 1226 ATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1285  
 Db 2768 ACTTCTCTGCTGCTTCTCCAAAGATTCATAATGCTGCTGCTGCTGCTGCTGCTGCTG 2827  
 QY 1286 TCTCCGAGTGGCCCATGATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1345  
 Db 2828 TATCTGCTGTAGTACACAAATATGCTTGGCTGTTGCTGCTGCTGCTGCTGCTGCTGCT 2887  
 QY 1346 TCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1405  
 Db 2888 TGTTCGCTCTTCATGCTTCTTGGAAATGCTTGGAAATGCTTCAACTTCATGCTGCTGCT 2947  
 QY 1406 CCGGCCCGCATGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465  
 Db 2948 AAAAGCCGATTTGGAATGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3007  
 QY 1466 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1510  
 Db 3008 TCTGCTTTTATCTCAAGAAATGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3052

RESULT 10

US-08-121-057-1

; Sequence 1, Application US/08121057

; Patent No. 5484727

; GENERAL INFORMATION:

; APPLICANT: CHANG, TA-YUAN

; APPLICANT: CHANG, CATHERINE C. Y.

; TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MA

|  |     |   |     |
|--|-----|---|-----|
| Db   | 862 | ATCCCACTGTAAGATGGGGTTATGTTGCTATCAAGTTTGCACAGGCTCTTTGGTGCCTTT  | 921 |
| QY   | 926 | TCATGCGCTTCATCTGGCGCCCTCTGTGTTCTCTTTCGCCAACAATGAGCCGAG        | 985 |
| Db   | 922 | TCATGCTACTACATCTTTGAAAGGCTTTGGCCCCCTTTTTCGGNAATATCAACAGG      | 981 |
| QY   | 986 | AGCCCTTCAGCACCC 1000  |     |
| Db   | 982 | AGCCCTTCAGCGCTC 996   |     |
| RESULT 11  |     |   |     |
| US-08-509-187D-1   |     |   |     |
| Sequence 1, Application US/08509187D                             |     |   |     |
| Patent No. 5834283   |     |   |     |
| GENERAL INFORMATION:   |     |   |     |
| APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.              |     |   |     |
| TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase |     |   |     |
| NUMBER OF SEQUENCES: 9   |     |   |     |
| CORRESPONDENCE ADDRESS:  |     |   |     |
| ADDRESSEE: LAHIVE & COCKFIELD, LLP                               |     |   |     |
| STREET: 28 State Street  |     |   |     |
| CITY: Boston   |     |   |     |
| STATE: Massachusetts   |     |   |     |
| COUNTRY: USA   |     |   |     |
| ZIP: 02109   |     |   |     |
| COMPUTER READABLE FORM:  |     |   |     |
| MEDIUM TYPE: Floppy disk   |     |   |     |
| COMPUTER: IBM PC compatible                                      |     |   |     |
| OPERATING SYSTEM: PC-DOS/MS-DOS                                  |     |   |     |
| SOFTWARE: PatentIn Release #1.0, Version #1.25                   |     |   |     |
| CURRENT APPLICATION DATA:  |     |   |     |
| APPLICATION NUMBER: US/08/509,187D                               |     |   |     |
| FILING DATE: 31-JUL-1995   |     |   |     |
| CLASSIFICATION: 435  |     |   |     |
| PRIOR APPLICATION DATA:  |     |   |     |
| APPLICATION NUMBER:  |     |   |     |
| FILING DATE:   |     |   |     |
| ATTORNEY/AGENT INFORMATION:                                      |     |   |     |
| NAME: Lamport Hammitte, Ann                                      |     |   |     |
| REGISTRATION NUMBER: 34,858                                      |     |   |     |
| REFERENCE/DOCKET NUMBER: DCI-033cpdv                             |     |   |     |
| TELECOMMUNICATION INFORMATION:                                   |     |   |     |
| TELEPHONE: (617)227-7400   |     |   |     |
| TELEFAX: (617)742-4214   |     |   |     |
| INFORMATION FOR SEQ ID NO: 1:                                    |     |   |     |
| SEQUENCE CHARACTERISTICS:  |     |   |     |
| LENGTH: 996 base pairs   |     |   |     |
| TYPE: nucleic acid   |     |   |     |
| STRANDEDNESS: single   |     |   |     |
| TOPOLOGY: linear   |     |   |     |
| MOLECULE TYPE: cDNA  |     |   |     |
| US-08-509-187D-1   |     |   |     |
| Query Match  |     |   |     |
| Best Local Similarity 53.1%;                                     |     |   |     |
| Score 134.6; DB 2; Length 996;                                   |     |   |     |
| Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps     |     |   |     |
| QY   | 287 | CATCCCTGGGGAACAGAAAGTTTTCATATCGCAAGTCCCTGCTTGATGAGCTCATGG     | 346 |
| Db   | 262 | CACCTCCAGAACAAAGAAAGATTTTATTCGAAGGCGCTCTCTCTTAGATGAATGCTTG    | 321 |
| QY   | 347 | AGGTGACAGATTTCGGACCATCTACACATGTTTCATCGTGGCTGTGTGCTTCATCA      | 406 |
| Db   | 322 | AAGTGGACCATCAGAACATATATCACATGTTTATTCGCTCCCTCATTCCTTTATCC      | 381 |
| QY   | 407 | TCAGACCCCTGGCCATCGACTTCATTGATGAGGCGAGGCTGCTGCTGG---AGTTTGACCT | 464 |
| Db   | 382 | TCAGACACTTGTAGTAGATTACATTGATGAAGGAGGCTGGTCTTGCAAGTTACGCTT     | 441 |
| QY   | 465 | ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGTGCCCATGTTTC   | 523 |
| Db   | 442 | CCTGCTTATGCATTTTGGCAAAATTCCTACCCGTTGTTTGGACCTGGTGATCATGTTTC   | 501 |



;; TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)

;; NUMBER OF SEQUENCES: 9

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: ASCII Text

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US93/09704A

;; FILING DATE: October 12, 1993

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: U.S. SER. NO. 959,950

;; FILING DATE: October 14, 1992

;; APPLICATION NUMBER: U.S. SER. NO. 121,057

;; FILING DATE: September 10, 1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: LAMPORT HAMMITTE, ANN.

;; REGISTRATION NUMBER: 34,858

;; REFERENCE/DOCKET NUMBER: DCI-033CP

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617) 227-5941

;; TELEFAX: (617) 227-5941

;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 996 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: cDNA

;; PCT-US93-09704A-1

Query Match 8.6%; Score 134.6; DB 5; Length 996;

Best Local Similarity 53.1%; Pred. No. 2.6e-25;

Matches 390; Conservative 0; Mismatches 324; Indels 21; Gaps 4;

Qy 287 CATCCCTGGGAAACAGAAAGTTTTCATATCCGCAAGTCCCTCTGATGAGCTGATGG 346

Db 262 CACCTCCAGAACAAAGATTTTATTGCAAGGCGCTCTCTTAGATGAAGTGTG 321

Qy 347 AGGTGCAGCATTTCCGACCATCTACCATGTTTCATGCTGGCTGTGTCTTCATCA 406

Db 322 AAGTGGACCATCAGAACAAATATACATGTTTATGCGCCTCTCATCTCTTTATCC 381

Qy 407 TCAGCACCTGGCCATGACTTCATTGATGAGGCAAGCTGCTGCTGG--AGTTTGACCT 464

Db 382 TCAGCACACTTGTAGTACATTACATTGATGAAGGAGGCTGGTCTTCAAGTTACGCT 441

Qy 465 ACTG-ATCTTCAGCTTCGACAGCTGCCATTTGGCGCTGGTGCACCTGGTGCCCATGTT 523

Db 442 COTGTCTTATGCATTTTGGCAAAATTCCTACCGTTGTTGGACCTGGTGGATCATGTTC 501

Qy 524 TGTCACACCTGTGGCGCGCTACAGGCGCTACGCGCTGTGGCGGAGGCGACCTGGAGCG 583

Db 502 TGCTACATTTTCAGTTCCTTATTTCTTTCATATTGGCGACCTGGCTATAGCAAGA 561

Qy 584 AGGCGACGGGCTCGGCTGTGCGCTTTTTCAGCGCCACCGCTGGTGCTC----- 633

Db 562 GTTCTCATCCGCTGATCGCTTCTCTCTCCATGGCTTTCTTTTATGATCTTCCAGATTG 621

Qy 634 ----TCGCGGCTCCGCTTCAGTGGCGCTGGAGCATACAGCTCCCGCGGCTCCCGTGT 690

Db 622 GAGTCTTAGTTTGGACCAACATATGTTGTTAGCATATCCTGGACCAAGCTTCCCGG 681

Qy 691 GTCCTGGTCTTCGACAGTGTAGTTCTCTGATGAAGAACTACTCTCTCTCTGAGAGGCT 750

Db 682 TTTATCATATTTCGAGCAGATCGTTTGTATGAGGCCCACTCATTTTGTTCAGAGAAC 741

Qy 751 GTGCTCGGATCTTCGTGCCAGACAGGATGAGGGATCCAGGCC-----CCAGTTTCT 805

Db 742 GTGCTCGGCTACTAATTCAGCTAAGGAGAAATCAAGCACTGTTTCCAAATACCTACAGTCA 801

Qy 806 CCAGCTACCTCTACTTCTCTCTGCCCCAACACTCATCTACAGGGAGACTTACCTAGGA 865

Db 802 ACCAGTATTGTACTTCTTATTGTCTTACCTTATCTACCTGACAGCTATCCAGGA 861

Qy 866 CCGCCTATGTCAGGTGGAATTATGTGGCAAGAACTTTGCCAGGCCCTGGGATGTGTC 925

Db 862 ATCCCACTGTAAGATGGGGTTATGTGCTATGAAGTTGCACAGGCTTTGGTGTCTTT 921

Qy 926 TCTATGCCCTTCATCTCTGGCGGCTCTGTGTCTCTCTTTCGCAACATGAGCCGAG 985

Db 922 TCTATGTGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTTGTCGGAATATCAACAGG 981

Qy 986 AGCCTTCAGCACCC 1000

Db 982 AGCCTTCAGCGCTC 996

#### RESULT 14

US-09-326-203A-14

; Sequence 14, Application US/09326203A

; Patent No. 644876

; GENERAL INFORMATION:

; APPLICANT: Lassner, Mike

; APPLICANT: Ruezinsky, Diane

; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic

; TITLE OF INVENTION: Acid Sequences

; FILE REFERENCE: 17045/00/WO

; CURRENT APPLICATION NUMBER: US/09/326,203A

; CURRENT FILING DATE: 1999-06-04

; PRIOR APPLICATION NUMBER: 60/088,143

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: 60/108,389

; PRIOR FILING DATE: 1998-11-12

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 1895

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (209)

; OTHER INFORMATION: n at position 209 is unknown

US-09-326-203A-14

Query Match 6.1%; Score 95; DB 4; Length 1895;

Best Local Similarity 58.7%; Pred. No. 4.9e-15;

Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

Qy 1019 TCCTGTCATGCCAGCTTCCAGGCATCTTCATGCTGCTGCTCATCTCTTTTGCCTTCCTCC 1078

Db 913 TCCTGAAGCTGGCGGTCCCAATCACCTCATCTGGCTCATCTTCTACTGGCTCTTCC 972

Qy 1079 ATTGCTGGCTCAAGCCCTTTGGCGAGATGTACGATTGGAGACAGGATTTCTACCGGG 1138

Db 973 ACTCCTGCCTGAATGCGGTGCTGAGCTCATGCACTGAGTTTGGAGACCGGGAGTTTACCGGG 1032

Qy 1139 ACTGGTGGAACTCAACCTCTCTTCCAACTACTACCCGACTTGGAACTGGTGTCCATG 1198

Db 1033 ACTGGTGGAACTCCGAGTGTCTACCTACTTCTGGCAGAACTGGAACTCCCTGTGCA 1092

Qy 1199 ACTGGCTGTACAGCTAGCTGTATCAGGATGGCTGGCGCTCTTGTGTGCCCGCCCGAG 1258

Db 1093 AGTGGTGCATCAGACACTTCTACAGGCCCATGCTTCGAC-----GGGCGACGAGCAAGT 1146

Qy 1259 GGGTAGCCATGCTGGGTGTGTCTCTGCTCCGAGTGGGCCCATGAGTATATCTTCTGCT 1318

Db 1147 GGATGGCCAGACAGGGGTGTCTCTGGCCTCGGCTTCTTCCACGAGTACCTGTGTGAGCG 1206

Qy 1319 TCGTCTGGGTTTCTTC 1335

Db 1207 TCCCTCTGCGAATGTTTC 1223

RESULT 15  
US-09-165-042-2  
; Sequence 2, Application US/09165042  
; Patent No. 6100077  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.  
; APPLICANT: Oelkers, Peter  
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL  
; TITLE OF INVENTION: ACYLTRANSFERASE  
; FILE REFERENCE: 0575/56331  
; CURRENT APPLICATION NUMBER: US/09/165.042  
; CURRENT FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1976  
; TYPE: DNA  
; ORGANISM: Yeast  
US-09-165-042-2

Query Match 6.1%; Score 95; DB 3; Length 1976;  
Best Local Similarity 58.7%; Pred. No. 5e-15;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;  
Qy 1019 TCCTGCATGCCAGCGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTCTTGCCTTCCTCC 1078  
Db 1212 TCCTGAAGCTGGCGTCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGGCTCTTCC 1271  
Qy 1079 ATTGCTGGCTCAACGCCCTTTCGCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGG 1138  
Db 1272 ACTCTGCGCTGAATGCCGCTGGCTGAGCTCATGCACTTTGGAGACCGGGAGTTCTACCGGG 1331  
Qy 1139 ACTGTTGGAACCTCAACGCTCTTCTCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198  
Db 1332 ACTGTTGGAACCTCCAGTCTGTCACCTACTTTCGCACAACTGGAACTCCCTGTGCACA 1391  
Qy 1199 ACTGCTGTACAGCTACGTGTATCAGATGGCTGGCTGCTCTTGGTCCCGGGCCCGAG 1258  
Db 1392 AGTGTGTCATCAGACACTTCTACAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 1445  
Qy 1259 GGGTAGCCATGCTGGTGTCTTCTGGTCTCGGAGTGGCCCATGATATATCTTCTGCT 1318  
Db 1446 GATGGCCAGGACAGGGGTGTCTTGGCTCGGCTTCTTCCACGAGTACCTGGTGAGCG 1505  
Qy 1319 TCGTCTGGGGTCTTC 1335  
Db 1506 TCCCTCTCGGAATGTC 1522

Search completed: April 30, 2003, 14:37:38  
Job time : 95 secs

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 14:09:11 ; Search time 141 Seconds  
(without alignments)  
13148.677 Million cell updates/sec

Title: US-09-918-026a-3  
Perfect score: 1569  
Sequence: 1 atggagccaggcggggccg.....cttggtctgcatacctag 1569

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 745064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                           |
|------------|-------|-------------|--------|-------|---------------------------------------|
| 1          | 403.6 | 25.7        | 418    | 9     | US-09-918-995-33158 Sequence 33158, A |
| 2          | 391   | 24.9        | 399    | 9     | US-09-918-995-33281 Sequence 33281, A |
| 3          | 387.2 | 24.7        | 401    | 9     | US-09-918-995-33355 Sequence 33355, A |
| 4          | 386   | 24.6        | 402    | 9     | US-09-918-995-33444 Sequence 33444, A |
| 5          | 385.6 | 24.6        | 401    | 9     | US-09-918-995-33843 Sequence 33843, A |
| 6          | 384   | 24.5        | 393    | 9     | US-09-918-995-33739 Sequence 33739, A |
| 7          | 376.2 | 24.0        | 401    | 9     | US-09-918-995-33159 Sequence 33159, A |
| 8          | 350.6 | 22.3        | 365    | 9     | US-09-918-995-34424 Sequence 34424, A |
| 9          | 350.6 | 22.3        | 408    | 9     | US-09-918-995-34099 Sequence 34099, A |
| 10         | 338.2 | 21.6        | 383    | 9     | US-09-918-995-35056 Sequence 35056, A |
| 11         | 138.8 | 8.8         | 471    | 9     | US-09-918-995-33288 Sequence 33288, A |
| 12         | 95    | 6.1         | 993    | 10    | US-09-764-853-79 Sequence 79, Appl    |
| 13         | 95    | 6.1         | 1411   | 9     | US-10-273-438-1 Sequence 1, Appl      |
| 14         | 95    | 6.1         | 1895   | 9     | US-10-157-855-14 Sequence 14, Appl    |
| 15         | 93.8  | 6.0         | 542    | 9     | US-09-764-868-587 Sequence 587, App   |
| 16         | 92.4  | 5.9         | 774    | 9     | US-09-764-868-279 Sequence 279, App   |
| 17         | 81.4  | 5.2         | 447    | 9     | US-09-918-995-29256 Sequence 29256, A |
| 18         | 81.4  | 5.2         | 452    | 10    | US-09-867-701-4664 Sequence 4664, Ap  |
| 19         | 81.4  | 5.2         | 1650   | 9     | US-10-273-438-3 Sequence 3, Appl      |

|    |      |     |      |    |                     |                   |
|----|------|-----|------|----|---------------------|-------------------|
| 20 | 81.4 | 5.2 | 1650 | 9  | US-10-273-438-9     | Sequence 9, Appl  |
| 21 | 80   | 5.1 | 1122 | 9  | US-09-774-639-29    | Sequence 29, Appl |
| 22 | 80   | 5.1 | 1122 | 9  | US-09-969-730-58    | Sequence 58, Appl |
| 23 | 79.8 | 5.1 | 1766 | 9  | US-10-157-855-15    | Sequence 15, Appl |
| 24 | 79.8 | 5.1 | 1766 | 9  | US-10-157-855-16    | Sequence 16, Appl |
| 25 | 70.2 | 4.5 | 1572 | 9  | US-10-223-076-17    | Sequence 17, Appl |
| 26 | 67.6 | 4.3 | 1181 | 9  | US-10-223-076-12    | Sequence 12, Appl |
| 27 | 57.8 | 3.7 | 2099 | 9  | US-10-223-076-11    | Sequence 11, Appl |
| 28 | 55.4 | 3.5 | 519  | 9  | US-09-918-995-1579  | Sequence 1579, Ap |
| 29 | 54.2 | 3.5 | 471  | 9  | US-10-223-076-14    | Sequence 14, Appl |
| 30 | 53.6 | 3.4 | 1964 | 9  | US-10-223-076-4     | Sequence 4, Appl  |
| 31 | 52.6 | 3.4 | 1537 | 9  | US-10-223-076-6     | Sequence 6, Appl  |
| 32 | 52.4 | 3.3 | 1446 | 9  | US-10-223-076-8     | Sequence 8, Appl  |
| 33 | 52.4 | 3.3 | 1512 | 9  | US-10-223-076-2     | Sequence 2, Appl  |
| 34 | 50   | 3.2 | 1904 | 9  | US-10-223-076-1     | Sequence 1, Appl  |
| 35 | 50   | 3.2 | 1942 | 9  | US-10-223-076-10    | Sequence 10, Appl |
| 36 | 49   | 3.1 | 2090 | 9  | US-09-770-791-192   | Sequence 192, App |
| 37 | 47.8 | 3.0 | 380  | 10 | US-09-764-853-314   | Sequence 314, App |
| 38 | 45.8 | 2.9 | 433  | 10 | US-09-878-574-15694 | Sequence 15694, A |
| 39 | 43.8 | 2.8 | 275  | 10 | US-10-123-155-204   | Sequence 204, App |
| 40 | 41.8 | 2.7 | 790  | 9  | US-09-815-242-7720  | Sequence 7720, Ap |
| 41 | 41.8 | 2.7 | 2802 | 10 | US-09-712-363-101   | Sequence 101, App |
| 42 | 41.2 | 2.6 | 2715 | 9  | US-10-123-153-10    | Sequence 10, Appl |
| 43 | 40.6 | 2.6 | 594  | 9  | US-09-866-562-60    | Sequence 60, Appl |
| 44 | 40.6 | 2.6 | 1089 | 10 | US-09-866-562-59    | Sequence 59, Appl |
| 45 | 40.6 | 2.6 | 1176 | 10 | US-09-866-562-59    | Sequence 59, Appl |

ALIGNMENTS

RESULT 1  
US-09-918-995-33158  
; Sequence 33158, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33158  
; LENGTH: 418  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-33158

|                       |        |   |           |            |        |        |    |      |    |
|-----------------------|--------|---|-----------|------------|--------|--------|----|------|----|
| Query Match           | 25.7%  | Score   | 403.6;    | DB-9;      | Length | 418;   |    |      |    |
| Best Local Similarity | 99.0%; | Pred. No.   | 2.8e-110; |            |        |        |    |      |    |
| Matches               | 406;   | Conservative  | 0;        | Mismatches | 4;     | Indels | 0; | Gaps | 0; |
| QY                    | 1122   | CAGGATGTTTCTACCGGACTGGTGGAACTCAACGTCCTCTCTCCAACTACTACCGCACTTG | 1181      |            |        |        |    |      |    |
| Db                    | 9      | CAGGATGTTTCTACCGGACTGGTGGAACTCAACGTCCTCTCTCCAACTACTACCGCACTTG | 68        |            |        |        |    |      |    |
| QY                    | 1182   | GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGGCGCTCCT  | 1241      |            |        |        |    |      |    |
| Db                    | 69     | GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGGCGCTCCT  | 128       |            |        |        |    |      |    |
| QY                    | 1242   | TGCTGGCCGGCCCGAGGGGTAGCCATGCTGGGTGTGTCTCTGCTCTCCGAGTGGGCCA    | 1301      |            |        |        |    |      |    |
| Db                    | 129    | TGCTGGCCGGCCCGAGGGGTAGCCATGCTGGGTGTGTCTCTGCTCTCCGAGTGGGCCA    | 188       |            |        |        |    |      |    |
| QY                    | 1302   | TGAGTATATCTTCTGCTTCTGCTCGTGGGGTTCCTATATCCGCTCATGCTGATCTCTTCCT | 1361      |            |        |        |    |      |    |
| Db                    | 189    | TGAGTATATCTTCTGCTTCTGCTCGTGGGGTTCCTATATCCGCTCATGCTGATCTCTTCCT | 248       |            |        |        |    |      |    |
| QY                    | 1362   | TGTCATTGGAGGAATGTTGAATTCATGATGATGATGATGATGATGATGATGATGATGATG  | 1421      |            |        |        |    |      |    |



Best Local Similarity 98.7%; Pred. No. 4.9e-105;  
Matches 389; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGACTGGTGAACACTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181  
Db 9 CAGGATGTTCTACCGGACTGGTGAACACTCAACGTCCTTCTCCAACTACTACCGCACTTG 68

Qy 1182 GAACGTGGTGCTTCCATGACTGGCTGTACAGCTTACGTGTATCAGGATGGCTGCGGCTCCT 1241  
Db 69 GAACGTGGTGCTTCCATGACTGGCTGTACAGCTTACGTGTATCAGGATGGCTGCGGCTCCT 128

Qy 1242 TGGTCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 1301  
Db 129 TGGTCCCGGGCCCGAGGGGTAAACCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 188

Qy 1302 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248

Qy 1362 TGTCAATTGAGGAATGTTGAACCTTCATGATGACGACCGCACCGGCGCATGGAA 1421  
Db 249 TGTCAATTGAGGAATGTTGAACCTTCATGATGACGACCGCACCGGCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACGACCGGCGCACTGCCCTTAC 1515  
Db 369 GGAGTGGTACGACCGGCGCACTGCCCTTAC 400

## RESULT 5

US-09-918-995-33843  
; Sequence 33843, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33843  
; LENGTH: 401  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-33843

Query Match 24.6%; Score 385.6; DB 9; Length 401;  
Best Local Similarity 99.0%; Pred. No. 6.4e-105;  
Matches 388; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGACTGGTGAACACTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181  
Db 9 CAGGATGTTCTACCGGACTGGTGAACACTCAACGTCCTTCTCCAACTACTACCGCACTTG 68

Qy 1182 GAACGTGGTGCTTCCATGACTGGCTGTACAGCTTACGTGTATCAGGATGGCTGCGGCTCCT 1241  
Db 69 GAACGTGGTGCTTCCATGACTGGCTGTACAGCTTACGTGTATCAGGATGGCTGCGGCTCCT 128

Qy 1242 TGGTCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 1301  
Db 129 TGGTCCCGGGCCCGAGGGAACCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 188

Qy 1302 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248

Qy 1362 TGTCAATTGAGGAATGTTGAACCTTCATGATGACGACCGCACCGGCGCATGGAA 1421  
Db 249 TGTCAATTGAGGAATGTTGAACCTTCATGATGACGACCGCACCGGCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACGACCGGCGCACTGCCCTTAC 1515  
Db 369 GGAGTGGTACGACCGGCGCACTGCCCTTAC 400

## RESULT 6

US-09-918-995-33739  
; Sequence 33739, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33739  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(393)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-33739

Query Match 24.5%; Score 384; DB 9; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1.9e-104;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTCTACCGGACTGGTGAACACTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181  
Db 9 CAGGATGTTCTACCGGACTGGTGAACACTCAACGTCCTTCTCCAACTACTACCGCACTTG 68

Qy 1182 GAACGTGGTGCTTCCATGACTGGCTGTACAGCTTACGTGTATCAGGATGGCTGCGGCTCCT 1241  
Db 69 GAACGTGGTGCTTCCATGACTGGCTGTACAGCTTACGTGTATCAGGATGGCTGCGGCTCCT 128

Qy 1242 TGGTCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 1301  
Db 129 TGGTCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGAGTGGCCCA 188

Qy 1302 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 1361  
Db 189 TGAGTATATCTTCTGCTTCGCTGGGTCTTCTATCCCGTCATGCTGATCTTCTCT 248

Qy 1362 TGTCAATTGAGGAATGTTGAACCTTCATGATGACGACCGCACCGGCGCATGGAA 1421  
Db 249 TGTCAATTGAGGAATGTTGAACCTTCATGATGACGACCGCACCGGCGCATGGAA 308

Qy 1422 CGTCTGATGTGGACCATGCTGTTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 1481  
Db 309 CGTCTGATGTGGACCATGCTGTTTTCTAGGCCAGGGAATCCAGGTACGCTGTACTGCCA 368

Qy 1482 GGAGTGGTACGACCGGCGCACTG 1505  
Db 369 GGAGTGGTACGACCGGCGCACTG 392

## RESULT 7

US-09-918-995-33159

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; Sequence 33159, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33159
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-33159

Query Match      24.0%; Score 376.2; DB 9; Length 401;
Best Local Similarity 98.7%; Pred. No. 4.1e-102;
Matches 389; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1122 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 1181
Db      9 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 68

QY 1182 GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTTACAGTATCAGATGGCTCGGCTCCT 1241
Db      69 GAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTTACAGTATCAGATGGCTCGGCTCCT 128

QY 1242 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTTCCTCCGCACTGGCCCA 1301
Db      129 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTTCCTCCGCACTGGCCCA 188

QY 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCCTTCTATCCCGTCATGCTGATCTCTTCT 1361
Db      189 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCCTTCTATCCCGTCATGCTGATCTCTTCT 248

QY 1362 TGTCATTGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGATGAT 1421
Db      249 TGTCATTGGAGGAATGTTGAACCTTCATGATGATGATGATGATGATGATGATGATGATGAT 308

QY 1422 CGTGTGATGTGGACCATGCTGTTTCTAGCCAGGGAATCCAGGTCAGGCTGTACTG 1478
Db      309 CGTGTGATGTGGACCATGCTGTTTCTAGCCAGGGAATCCAGGTCAGGCTGTACTG 365

RESULT 9
US-09-918-995-34099
; Sequence 34099, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34099
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-34099

Query Match      22.3%; Score 350.6; DB 9; Length 408;
Best Local Similarity 94.9%; Pred. No. 1.7e-94;
Matches 373; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1122 CAGGATGTTCTACCGGACCTGGTGAACCTCAAGCTCCTCTCCAACTACTACCGCACTTG 1181
Db      15 CCGGATTTTCTACCGGACCTGGGGGAACCTCAACGTTCTTCTTCAACTACTACCGCACTTG 74

QY 1182 GAACGTGGTGGTCCATGACTGGCTGTACAGCTAGCTATCAGATGGCTCGGCTCCT 1241
Db      75 GAACGTGGTGGTCCATGACTGGCTGTACAGCTAGCTATCAGATGGCTCGGCTCCT 134

QY 1242 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTTCCTCCGCACTGGCCCA 1301
Db      135 TGGTGCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTTCTTCCTCCGCACTGGCCCA 194

QY 1302 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCCTTCTATCCCGTCATGCTGATCTCTTCT 1361
Db      195 TGAGTATATCTTCTGCTTCGCTCGCTGGGTTCCTTCTATCCCGTCATGCTGATCTCTTCT 254
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Qy 1362 TGTCAATTGGAGAAATGTTGAACCTTCATGATGATGACGAGCGCACCGCCGGCATGGAA 1421
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Db 255 TGTCAATTGGAGAAATGTTGAACCTTCATGATGATGACGAGCGCACCGCCGGCATGGAA 314
|||||
Qy 1422 CGTGTGTATGTTGACCATGTC-TGTTTCTAGGCCAGGGAATCCAGGTGACGCTGTACTGCC 1480
|||||
Db 315 CAGGTGTATGTTGACCATGTC-TGTTTCTAGGCCAGGGAATCCAGGTGACGCTGTACTGCC 374
|||||
Qy 1481 AGGAGTGTATGACGAGCGGCGGCACTGCCCTTAC 1513
|||||
Db 375 AAGAGTGTATGACGAGCGGCGGCACTGCCCTTAC 407
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RESULT 10
US-09-918-995-35056
; Sequence 35056, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35056
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(383)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-35056

Query Match 21.6%; Score 338.2; DB 9; Length 383;
Best Local Similarity 95.1%; Pred. No. 8.4e-91;
Matches 349; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1122 CAGGATGTTTACCGGGACTGGTGAACCTCAACGCTCTTCCCAACTACTACCGCACATG 1181
|||||
Db 9 CAGGATGTTTACCGGGACTGGTGAACCTCAACGCTCTTCCCAACTACTACCGCACATG 68
|||||
Qy 1182 GAACGTGTGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGCTCGGCTCCT 1241
|||||
Db 69 GAACGTGTGTGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGCTCGGCTCCT 128
|||||
Qy 1242 TGGTCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTGTCTCTGCTCCGCGAGTGGCCCA 1301
|||||
Db 129 TGGTCCCGGGCCCGAGGGGTAAACCATGCTGGGTGTGTCTCTGCTCCGCGAGTGGCCCA 188
|||||
Qy 1302 TGAGTATATCTTCTGCTTCGCTGGGGTCTTCTATCCGCTCATGCTGATCTTCTCT 1361
|||||
Db 189 TGAGTATATCTTCTGCTTCGCTGGGGTCTTCTATCCGCTCATGCTGATCTTCTCT 248
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Qy 1362 TGTCAATTGGAGAAATGTTGAACCTTCATGATGATGACGAGCGCACCGCCGGCATGGAA 1421
|||||
Db 249 TGTCAATTGGAGAAATGTTGAACCTTCATGATGATGACGAGCGCACCGCCGGCATGGAA 308
|||||
Qy 1422 CGTGTGTATGTTGACCATGTC-TGTTTCTAGGCCAGGGAATCCAGGTGACGCTGTACTGCCA 1481
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Db 309 CGTGTGTATGTTGACCATGTC-TGTTTCTAGGCCAGGGAATCCAGGTGACGCTGTACTGCCA 368
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Qy 1482 GGAGTGG 1488
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Db 369 CGAGTGG 375
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RESULT 11
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US-09-918-995-32388
; Sequence 32388, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32388
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32388

Query Match 8.8%; Score 138.8; DB 9; Length 471;
Best Local Similarity 92.4%; Pred. No. 2.4e-31;
Matches 146; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 883 AATTATGTGGCCCAAGAACTTTGCCAGGCGCTGGGATGTGCTCTATGCTCTTCATC 942
|||||
Db 168 AGTTATGTGTCCTCATGCCCCCTCCAGGCGCTGGGATGTGCTCTATGCTCTTCATC 227
|||||
Qy 943 CTGGGCGCGCTCTGTGTTCTCTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGT 1002
|||||
Db 228 CTGGGCGCGCTCTGTGTTCTCTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGT 287
|||||
Qy 1003 GCCCTGGTGTCTCTATCTTCATGCGATGCCAGTGGCCAGG 1040
|||||
Db 288 GCCCTGGTGTCTCTATCTTCATGCGATGCCAGTGGCCAGG 325
|||||

RESULT 12
US-09-764-853-79/c
; Sequence 79, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-79

Query Match 6.1%; Score 95; DB 10; Length 993;
Best Local Similarity 58.7%; Pred. No. 3.7e-18;
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

Qy 1019 TCCTGATGCCACGTTGCCAGGATCTTCATGCTGCTGCTCATCTCTCTTTGCTCTCC 1078
|||||
Db 780 TCCTGAAGCTGGCGTCCCAATCATCTGCTGCTCATCTCTCTTTGCTCTCTCC 721
|||||
Qy 1079 ATTGCTGGCTCAACGCTTTGCCGAGATGCTACGATTTTGGAGACAGGATTTTACCGGG 1138
|||||
Db 720 ACTCTGCTGAATGCCGTGGCTGAGCTCATGACGTTTGAGACCGGAGTTTACCGGG 661
|||||
Qy 1139 ACTGGTGGAACTCAACGCTCTTCTTCAACTACTACCGCACTTGGAACTGGTGGTCCATG 1198
|||||
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Db 660 ACTGGTGAACCTCCGAGTGTGTACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 601  
QY 1199 ACTGGGTGTACAGCTACGTGTATCAGATGGGTGGCTGGCTCTTGGTGGCCGGCCCGAG 1258  
Db 600 AGTGGTGCATCAGACACTTCTACAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 547  
QY 1259 GGATGACCATGCTGGTGTGTCTCTGGTCTCCGCACTGCGCCATGATGATATATCTTCTGCT 1318  
Db 546 GGATGGCCAGGACAGGGGTGTTCTGGCTCGCCCTTCTTCCAGAGTACCTGGTGAGCG 487  
QY 1319 TCCTCTCTGGGTCTTTC 1335  
Db 486 TCCCTCTGCGAATGTTTC 470

RESULT 13  
US-10-273-438-1  
; Sequence 1, Application US/10273438  
; Publication No. US20030072757A1  
; GENERAL INFORMATION:  
; APPLICANT: Farese, Robert V.  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Smith, Steven  
; APPLICANT: Erickson, Sandra  
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase  
; FILE REFERENCE: UCAL-105CIP2  
; CURRENT APPLICATION NUMBER: US/10/273,438  
; CURRENT FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US/10/040,315  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 60/107,771  
; PRIOR FILING DATE: 1998-11-09  
; PRIOR APPLICATION NUMBER: PCT/US98/17883  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 09/103,754  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 09/339,472  
; PRIOR FILING DATE: 1999-06-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-273-438-1

Query Match 6.1%; Score 95; DB 9; Length 1411;  
Best Local Similarity 58.7%; Pred. No. 4.2e-18;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGCATGCCACGTTGCCAGGCATTTTCATGCTGCTCATCTTCTTTTGGCTTCTCTCC 1078  
Db - 662 TCCTGAAGCTGGCGTCCCAATCACCTCATCTGCTCATCTTCTTCTACTGGCTCTTCC 721  
QY 1079 ATTGCTGCTCAAGCCCTTCCCGAGATGCTACCATTTGGAGCAGAGTGTCTTACCCGG 1138  
Db 722 ACTCCTGCTGAATGCCGTGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 781  
QY 1139 ACTGGTGAACCTCAACGCTTCTTCCAACTACTACCGCAGTGTGGAAGCTGGTGTCCATG 1198  
Db 782 ACTGGTGAACCTCCGAGTCTGTACCTACTTCTTGGCAGAACTGGAACATCCCTGTGCACA 841  
QY 1199 ACTGGCTGTACAGTACGTGTATCAGGATGGCTGCGGCTCTTGGTGGCCCGGCCCGAG 1258  
Db 842 AGTGGTGCATCAGACACTTCTACAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 895  
QY 1259 GGTAGCAGTCTGGTGTGTCTCTGGTCTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318  
Db 896 GGATGGCCAGGACAGGGGTGTTCTGGCTCGCCCTTCTTCCAGAGTACCTGGTGAGCG 955  
QY 1319 TCGTCTCTGGGTCTTTC 1335

Db 956 TCCCTCTCGGAATGTTTC 972

RESULT 14  
US-10-157-855-14  
; Sequence 14, Application US/10157855  
; Patent No. US20020170091A1  
; GENERAL INFORMATION:  
; APPLICANT: Lassner, Michael W.  
; APPLICANT: Ruzinsky, Diane M.  
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic  
; TITLE OF INVENTION: Acid Sequences  
; FILE REFERENCE: 16516.158  
; CURRENT APPLICATION NUMBER: US/10/157,855  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: 09/326,203  
; PRIOR FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: 60/088,143  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/108,389  
; PRIOR FILING DATE: 1998-11-12  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 1895  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (209)  
; OTHER INFORMATION: n at position 209 is unknown  
US-10-157-855-14

Query Match 6.1%; Score 95; DB 9; Length 1895;  
Best Local Similarity 58.7%; Pred. No. 4.7e-18;  
Matches 186; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

QY 1019 TCCTGCATGCCACGTTGCCAGGCATTTTCATGCTGCTCATCTTCTTCTTCTTCTTCTCC 1078  
Db 913 TCCTGAAGCTGGCGTCCCAATCACCTCATCTGCTCATCTTCTTCTTCTTCTTCTTCTCC 972  
QY 1079 ATTGCTGGCTCAACGCTTTCGCGAGATGCTACGATTTGGAGACAGATGTTCTTACCCGG 1138  
Db 973 ACTCCTGCTGATGCTGGTGGCTGAGCTCATGAGTTCGAGACCCGGAGTTCACCCGG 1032  
QY 1139 ACTGGTGAACCTCAACGCTTCTTCCAACTACTACCGCAGTTCGAGTGTGGTGTCCATG 1198  
Db 1033 ACTGGTGAACCTCCGAGTCTGTACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 1092  
QY 1199 ACTGGCTGTACAGCTAGTGTATCAGATGGCTGCGGCTGCTTGGTGGCCCGGCCCGAG 1258  
Db 1093 AGTGGTGCATCAGACACTTCTTACAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 1146  
QY 1259 GGATGACCATGCTGGGTGTGTCTTCTGGTGTCCGAGTGGCCCATGAGTATATCTTCTGCT 1318  
Db 1147 GGATGGCCAGGACAGGGGTGTTCTTGGCTCGCCCTTCTTCCAGAGTACCTGGTGAGCG 1206  
QY 1319 TCGTCTCTGGGTCTTTC 1335  
Db 1207 TCCCTCTCGGAATGTTTC 1223

RESULT 15  
US-09-764-868-587  
; Sequence 587, Application US/09764868  
; Patent No. US20020168711A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ32  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper

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: NUMBER OF SEQ ID NOS: 1510
: SOFTWARE: PatentIn ver. 2.0
: SEQ ID NO 587
:   LENGTH: 542
:   TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
:   NAME/KEY: SITE
:   LOCATION: (377)
:   OTHER INFORMATION: n equals a,t,g, or c
:   NAME/KEY: SITE
:   LOCATION: (397)
:   OTHER INFORMATION: n equals a,t,g, or c
:   NAME/KEY: SITE
:   LOCATION: (441)
:   OTHER INFORMATION: n equals a,t,g, or c
:   NAME/KEY: SITE
:   LOCATION: (507)
:   OTHER INFORMATION: n equals a,t,g, or c
: US-09-764-868-587

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| Query Match                  | 6.0%; Score 93.8; DB 9; Length 542;                                 |
|------------------------------|---|
| Best Local Similarity        | 58.8%; Pred. No. 6.6e-18;   |
| Matches 183; Conservative 0; | Mismatches 122; Indels 6; Gaps 1;                                   |
| QY 1019                      | TCCTGCATGCCACGTTGGCCAGGCATCTTCATGCTGCTGCTCATCTCTCTTTGGCTTCCTCC 1078 |
| Db                           |   |
| 54                           | TCCTGAAGCTGGCGGTCCCCAATCACTCATCTGGCTCATCTTCTTCTACTGGCTCTCTCC 113    |
| QY 1079                      | ATTGCTTGGCTCAACGGCTTTGGCCGAGATGCTACGATTTGGAGACAGGATCTTCTACCGGG 1138 |
| Db                           |   |
| 114                          | ACTCTCGCTGATGCGGTGGCTGAGCTCATGCACTTGGAGACCGGGAGTCTTACCGGG 173       |
| QY 1139                      | ACTGGTGGAACTCAACGTCTCTTCCAACCTACTACCGCACTTGGACGTTGGTTCCTCATG 1198   |
| Db                           |   |
| 174                          | ACTGGTGGAACTCCGAGTCTGTACACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA 233   |
| QY 1199                      | ACTGGCTGTACAGTACGTTGTATCAGGATGGCTGCGGCTCTCTTGGTGGCCGGGCCCGAG 1258   |
| Db                           |   |
| 234                          | AGTGGTGCATCAGACACTTCTAAGGCCATGTTCTGCAC-----GGGGCAGCAGCAAGT 287      |
| QY 1259                      | GGGTAGCCATGCTGGGTGTCTTCTGGTCTCCGACGTGGCCCATGAGTATATCTTCTGCT 1318    |
| Db                           |   |
| 288                          | GGATGCCAGGACAGGGGTCTTCTGGCCTCGGCTTCTTCCACGAGTACCTGGTGAGCG 347       |
| QY 1319                      | TCCTCTCTGGGG 1329   |
| Db                           |   |
| 348                          | TCCTCTGGCG 358  |

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Job time : 152 secs

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GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 13:03:20 ; Search time 1601 Seconds  
(without alignments)  
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Perfect score: 1569  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
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Maximum Match 100%  
Listing first 45 summaries

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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
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13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_Other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
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| 1          | 402.4 | 25.6        | 799    | 13    | BI222037           |
| 2          | 335.8 | 21.4        | 563    | 10    | BE236762           |
| 3          | 298.2 | 19.0        | 778    | 13    | BG920709           |
| 4          | 281.6 | 17.9        | 705    | 12    | BG105735           |
| 5          | 272.6 | 17.4        | 992    | 12    | BG674469           |
| 6          | 268   | 17.1        | 840    | 12    | BG529751           |
|            |       |             |        |       | BG529751 602560522 |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 7  | 264   | 16.8 | 893 | 9  | AL527439 | AL527439           |
| 8  | 246.2 | 15.7 | 694 | 9  | AA867129 | AA867129 vx23f11.r |
| 9  | 245   | 15.6 | 741 | 12 | BG696168 | BG696168 602659280 |
| 10 | 241.6 | 15.4 | 731 | 9  | A1049480 | A1049480 ub37ell.r |
| 11 | 240   | 15.3 | 300 | 9  | AU099137 | AU099137 AU099137  |
| 12 | 238.8 | 15.2 | 846 | 12 | BG500675 | BG500675 602547068 |
| 13 | 233.8 | 14.9 | 887 | 9  | AA867128 | AA867128 vx23f10.r |
| 14 | 227.6 | 14.5 | 635 | 17 | AG133295 | AG133295 Pan trolg |
| 15 | 222.4 | 14.2 | 848 | 12 | BG697784 | BG697784 602661272 |
| 16 | 221.8 | 14.1 | 810 | 12 | BF681650 | BF681650 602155732 |
| 17 | 221.2 | 14.1 | 746 | 12 | BG698372 | BG698372 602658292 |
| 18 | 216.4 | 13.8 | 960 | 12 | BG105756 | BG105756 602311984 |
| 19 | 214   | 13.6 | 682 | 12 | BG743201 | BG743201 602634363 |
| 20 | 213.2 | 13.6 | 420 | 9  | AA410072 | AA410072 EST02151  |
| 21 | 204.4 | 13.0 | 484 | 10 | AA466137 | AA466137 BP230022A |
| 22 | 204.2 | 13.0 | 553 | 10 | BE013288 | BE013288 123187 MA |
| 23 | 202   | 12.9 | 878 | 14 | BQ887458 | BQ887458 AGENCOURT |
| 24 | 200.2 | 12.8 | 608 | 9  | AA867781 | AA867781 vx16e09.r |
| 25 | 197.6 | 12.6 | 500 | 12 | BE861030 | BE861030 UI-M-AP1- |
| 26 | 186.2 | 11.9 | 601 | 14 | BQ200762 | BQ200762 UI-R-EB1- |
| 27 | 185.2 | 11.8 | 915 | 12 | BF968277 | BF968277 602269663 |
| 28 | 183   | 11.7 | 460 | 14 | R10272   | R10272 yf36b09.r1  |
| 29 | 181.2 | 11.5 | 876 | 12 | BF578775 | BF578775 602094805 |
| 30 | 177.6 | 11.3 | 510 | 9  | AL181841 | AL181841 un87n09.r |
| 31 | 175   | 11.2 | 376 | 10 | AA425878 | AA425878 58867 MAR |
| 32 | 171.8 | 10.9 | 655 | 10 | BE026601 | BE026601 db28h02.x |
| 33 | 169.8 | 10.8 | 883 | 12 | BG105795 | BG105795 602312644 |
| 34 | 167.8 | 10.7 | 590 | 9  | AL773907 | AL773907 AL773907  |
| 35 | 162.4 | 10.4 | 639 | 13 | BM485692 | BM485692 pgn1c.pk0 |
| 36 | 148.4 | 9.5  | 612 | 10 | BE025829 | BE025829 db28h02.y |
| 37 | 147.4 | 9.4  | 662 | 14 | BQ521546 | BQ521546 NISC_n111 |
| 38 | 147   | 9.4  | 801 | 12 | BF130076 | BF130076 601817955 |
| 39 | 143   | 9.1  | 385 | 10 | BB872762 | BB872762 BB872762  |
| 40 | 141.4 | 9.0  | 689 | 13 | BJ016863 | BJ016863 BJO16863  |
| 41 | 141.4 | 9.0  | 697 | 13 | BJ019808 | BJ019808 BJO19808  |
| 42 | 140.4 | 8.9  | 721 | 13 | BJ028057 | BJ028057 BJO28057  |
| 43 | 139.6 | 8.9  | 452 | 14 | W76421   | W76421 z867el2.r1  |
| 44 | 139.6 | 8.9  | 668 | 13 | BJ014628 | BJ014628 BJO14628  |
| 45 | 139.4 | 8.9  | 467 | 14 | R07295   | R07295 yf14e10.r1  |

# ALIGNMENTS

|            |  |  |
|------------|--|--|
| RESULT 1   | BI222037   | 602935989F1 NCI_GAP_L19 Mus musculus cDNA clone IMAGE:5099063 5', linear EST 11-JUL-2001 |
| LOCUS      | BI222037   | 799 bp mRNA  |
| DEFINITION | 602935989F1 NCI_GAP_L19 Mus musculus cDNA clone IMAGE:5099063 5', linear EST 11-JUL-2001   |  |
| ACCESSION  | BI222037   | mRNA sequence.   |
| VERSION    | BI222037   |  |
| KEYWORDS   | EST.   |  |
| SOURCE     | house mouse.   |  |
| ORGANISM   | Mus musculus   |  |
| REFERENCE  | 1 (bases 1 to 799)   |  |
| AUTHORS    | National Institutes of Health, Mammalian Gene Collection (MGC)   |  |
| TITLE      | National Institutes of Health, Mammalian Gene Collection (MGC)   |  |
| JOURNAL    | Unpublished (1999)   |  |
| COMMENT    | Contact: Robert Strausberg, Ph.D.<br>Email: cgabbs-r@mail.nih.gov<br>Tissue Procurement: Jeffrey E. Green, M.D.<br>CDNA Library Preparation: Life Technologies, Inc.<br>CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)<br>DNA Sequencing by: Incyte Genomics, Inc.<br>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:<br>http://image.llnl.gov<br>Plate: LLAM11238 row: b column: 24<br>High quality sequence start: 28<br>High quality sequence stop: 798.<br>Location/Qualifiers |  |

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source
1. 799
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5099063"
/clone_lib="NCI CGAP L19"
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: liver; Vector: PCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 176 a 217 c 247 g 158 t
ORIGIN
Query Match 25.6%; Score 402.4; DB 13; Length 799;
Best Local Similarity 78.7%; Pred. No. 1.8e-83;
Matches 524; Conservative 0; Mismatches 126; Indels 16; Gaps 3;

QY 28 CTGCAGAGACAGAGGGCTGGGAGGGGAGCGGCGCCACCCCTGT---GGAGATGGA 84
DB 133 CTTCCGAGGAGAGAGGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 192
QY 85 AACATGAGACGAC-AGAGCCCGGACTGTGTACATGACACCGACACATGGAGCTCT 143
DB 193 AACGCAAGGACACACTGGAAACCCAGACTTGGTGAATGGACTCGACATATGGAGCTGT 252
QY 144 GAAGGCACAAATTCGTGAGCAAGCGAGGAGCAACTGAGGGAGCTGCTGGATCGGGCCAT 203
DB 253 GAAGACACAGTTCTGGAGCAACACAGAGAGATTGGCAGAGCTGTGGATCGGGCCCT 312
QY 204 GCGGAGGCTATACATTCCTACCCATCAAGAGACAAACCTCTGCCGCCACCTCCCCAGG 263
DB 313 ATGGGAGGCTATGCAAGCTTACCCCAACAGACAGACCTCTTCCCTCCGCTCCCCAGA 372
QY 264 TTCCTTGAGCAGGACCCAGGAGCCATCCCTGGGGAACAGAAAGTTTTCATATCCGCAA 323
DB 373 TTCTACAAAGAACGACCAAGAGTTACCCCTGGAAACGGAAGTTTTCATACCCGCAA 432
QY 324 GTCCTCTGCTGATGAGCTGATGAGGTGACAGCATTTCCGACACCATCTACACATGTTTAT 383
DB 433 GTCACATGATGAGCTAATGAGGTGCAACATTTCCGAACCATCTACACATGTTTAT 492
QY 384 CGTGGGCTGTGTCTTATCATCAGCACCCCTGGCCATCGACTTCATTTGATAGGGCAG 443
DB 493 AGCGGGCTATGCTGCTGATCATCAGCACCCCTGGCCATCGACTTCATTTGATAGGGCAG 552
QY 444 GCTGCTGCTGAGTTTCACTACTGATCTTCACTTCCGACAGCTGCGCATTTGGCGTGT 503
DB 553 GTTGATGCTGAGTTTCACTACTGATCTTCACTTCCGACAGCTGCGCTTGGCGTGT 612
QY 504 GACCTGGGTGCCATGTTTCTGTCACCCCTGTTGGCCCGCTACAGGCCCTACGGCTGTG 563
DB 613 GACCTGGGTGCCATGTTTCTGTCACCCCTGTTGGCCCGCTACAGGCCCTACGGCTGTG 672
QY 564 GGCCA-----GGGCACTCGAGCGAGCGGCGGCGCTGGCGTGTGCGCTTTT 611
DB 673 GGCCAGGCGGCGGCTGGGGTGTCTGGATGCTGGGGCGGCGGCTGGCGTGTGCT 732
QY 612 AGCGGCGGCGGCGGCTGGGTGTCTGCGGCTGCGCGGTCCAGCTGGCGGCTGGAGCATCAGT 671
DB 733 GGCTGCCACGCTGTGGTGTCTGCGTCTGCGTCTGCGGCTGACGCTGTCAGTGGAGCTT 792
QY 672 CCGGC 677
DB 793 TCCGAC. 798.

RESULT 2
LOCUS BE236762 563 bp mRNA linear EST 25-APR-2001
DEFINITION 145578 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE236762
VERSION BE236762.1 GI:9021480

KEYWORDS SOURCE ORGANISM EST.
Bos taurus Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 563)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001).
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAG
Plate: 55 row: 0 column: 15
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1. 563
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/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/Note="Vector: PCMV SPORT6; Site:1: NotI; Site:2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."
BASE COUNT 129 a 160 c 170 g 103 t 1 others
ORIGIN
Query Match 21.4%; Score 335.8; DB 10; Length 563;
Best Local Similarity 85.6%; Pred. No. 5.9e-68;
Matches 373; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 82 GGAACACCTGAGACGACAGAGCCCGGAGCTTGGTACAATGGACCCGACACATGGAGCT 141
DB 128 GGAACCGGAGGTGCACAGAGGCCAGATTTGGTCAATGGACCCAGCATATGACGCT 187
QY 142 GTCAAGGCACATTTCTGGAGCAAGCGGACAGCACTGAGGAGCTGCTGGATCGGGC 201
DB 188 GTAAGACACAGTTGTGGAGCAAGCGGAGGCCAGCTGATGGAGCTGCTGGATCGGCC 247
QY 202 ATCGGGAGGCTATACAATCCTACCATCACAGACAAACCTCTGCCCCACCTCCCCCA 261
DB 248 ATGTGGGAGCAGTTCAAGCTTACCCACTGCAAGACAGACAGACAGCTCGCTCCGTC 307
QY 262 GGTTCCTTGAGAGGAGCCAGGAGCCATCCTGGGAAACAGAAAGTTTTCATCATCCGC 321
DB 308 GACTCCTTGGCGAAGACCCCGGAGCGTCCCTGGGGAAACGAAAGTTTTCATCATCCGC 367
QY 322 AAGTCCCTGCTGATGAGCTGATGGAGGTGACAGATTTCGCGACCATCTACCATGTTTC 381
DB 368 AAGTCCCTGCTTGACGAGCTGATGGAGGTGCGGAGCTTCCGACCATCTACCATATGTTT 427
QY 382 ATCGCTGGCCTGTGTCTTTCATCATCAGCACCCCTGGCCATCGACTTCATTTGATGAGGC 441
DB 428 GTCGCGGCGCTGTGTCTTTCATCATCAGCACCCCTGGCCATCGACTTCATTTGATGAGGC 487
QY 442 AGGCTGCTGTGGAGTTTGACCTACTGATGATCTTTCAGCTTCGAGCAGCTGCCATGGGCTG 501
DB 442 AGGCTGCTGTGGAGTTTGACCTACTGATGATCTTTCAGCTTCGAGCAGCTGCCATGGGCTG 501

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BASE COUNT      139 a      155 c      153 g      258 t
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Query Match      17.9%; Score 281.6; DB 12; Length 705;
Best Local Similarity 64.2%; Pred. No. 3.le-55;
Matches 439; Conservative 0; Mismatches 244; Indels 1; Gaps 1;
QY 843 CTACAGGAGACATACCTAGGAGCCCTATGTCAGGTGGAATATGTGGCCAAAGAACTT 902
DB 1 CTACCGTGACAGTATCCCAAGGAATCCCACTGAAGATGGGTATGTGCTATGAAGTT 60
QY 903 TGCCAGGCGCTGGGATGTGTCTATGCTCTTATCTTCATCTCGGCGCCCTCTGTCTTC 962
DB 61 TGCACAGGTCTTGGTGTCTTTCTATGTGTACTACATCTTTGAAGGCT-TGTGCCCG 119
QY 963 TGTCTTTGCCAATGACGAGCGGCTTACAGACCGGTGCTGCTCTCTATCT 1022
DB 120 CTTGTTTCGGAATATCAACAGAGGCCCTTCAGCGCTGCTGTCTGCTATGTAT 179
QY 1023 GCATGCCAGCTTGCAGGATCTTCATGCTGCTCATCTCTTTGCCCTTCCTCCATTG 1082
DB 180 TAATCCTATCTGCGAGGTGTGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
QY 1083 CTGCTCAAGCGCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTTACCGGACTG 1142
DB 240 CTGCTCAATGCCCTTGTCTGAGATGTTACGCTTTGGTGCAGAGATGTTCTATAAGGAT 299
QY 1143 GTGGAATCAACGCTCTTCCAACTACTACCGCACTTGGAACTGCTGTGCTCATGCTG 1202
DB 300 GTGGAATCCACGCTACTCTCAACTATATAGAACTGGAATGTGTGCTCATGCTG 359
QY 1203 GCTGTACAGCTACGTATCAGGATGGGCTCGGCTCTCTTGGTCCGCGCCGCGAGGGT 1262
DB 360 GCTATATCTACTGCTTACAGGACTTCTCTGCTTTTCTTCCAAAGAGATTCAAATCTGC 419
QY 1263 AGCATGCTGGGTGTTCTGCTGCTCGGAGTGGCCCATGATATCTCTCTCTCTCT 1322
DB 420 TGCCATGTTAGCTGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
QY 1323 CTGCGGCTCTCTATCCCGCTCATGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 1382
DB 480 CTGAGCTTTTCTATCCCGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 539
QY 1383 CTTCTATGATGATGACGACGACGCGCGCGGATGGAACGTGCTGATGTGGACCATGCT 1442
DB 540 CTTCTATGCTCAATGATAGTCAAGAAAGCCGATTTGGAATGCTGATGTGGACTTCTCT 599
QY 1443 GTTTCTAGCCAGGAATCCAGGTACAGCTGCTACTGCTCAGGAGTGGTACGACGCGGCA 1502
DB 600 TTTCTGGGCAATGAGTCTTACTCTGCTTTTATCTCAAGAAATGGTATGACGCTCAGCA 659
QY 1503 CTGCGCTTACCCAGCAACTTT 1526
DB 660 CTGCTCTGAAATCCACATTT 683
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LOCUS 992 bp mRNA linear EST 01-MAY-2001
DEFINITION mRNA sequence.
ACCESSION BG674469
VERSION BG674469.1 GI:13905865
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 992)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10593 row: n column: 22  
High quality sequence stop: 828.  
Location/Qualifiers  
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/clone="IMAGE:4746069"  
/clone\_lib="NCI\_CGAP\_Skn3"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: skin; Vector: PCMV-SPORT6; Site: 1; NotI;  
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 199 a 216 c 231 g 346 t  
ORIGIN

Query Match 17.4%; Score 272.6; DB 12; Length 992;  
Best Local Similarity 63.2%; Pred. No. 4.6e-53;  
Matches 419; Conservative 0; Mismatches 244; Indels 0; Gaps 0;  
QY 901 TTGCCCAGCGCTGGGATGTGTCTATGCTGCTTCTCATCTGCTGCGCGCCCTCTGTGT 960  
DB 2 TTGTCACAGTCTTGTGCTTTTCTATGTACTACATCTTTGAAAGGCTTTGTGCC 61  
QY 961 CTTGCTTTTCCAAATGAGCCGAGAGCCCTTCAGCACCGCTGCTGCTCTCTATC 1020  
DB 62 CCCTGTTTGGGAATATCAACAGGAGCCCTTCAGCGCTGCTGCTGCTGCTATGTA 121  
QY 1021 CTGCATCCAGCTTGCAGGCATCTTCATGCTGCTGCTCTCTCTCTCTCTCTCTCT 1080  
DB 122 TTTAACTCCATCTGCCAGGTGTGCTGATCTCTCTCTCTCTCTCTCTCTCTCT 181  
QY 1081 TGTGCTCAACCGCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAC 1140  
DB 182 TGTGCTCAATGCCTTGTGCTGAGATGTTACGCTTTTGGTACAGGATGTTCTATAAGGAT 241  
QY 1141 TGTGGAACCTCAACGCTCTCTCCACTACTACCGCACTTGGAACTGGTGGTCCATGAC 1200  
DB 242 TGTGGAACCTCCAGCTCATCTCCAACTATATAGAACCTGGAATGTGGTGGTCCATGAC 301  
QY 1201 TGGCTGTACAGCTACGTGTATCAGGATGGCTGCGGCTCCTTGGTCCCGCGCCGAGGG 1260  
DB 302 TGGCTATATTACTATGCTTACAAGGACTTTCTCTGGTTTCTCTCAAGAGATTCAAATCT 361  
QY 1261 GTAGCCATGCTGGGTGTGTTCTCGGAGTGTCCGAGTGCCCATGATATATCTTCTGCTTC 1320  
DB 362 GCTGCCATGTAGCTGCTTTGCTGTATCTGCTGTAGTACAGAAATATGCTTTGGCTGTT 421  
QY 1321 GTCTGGGGTCTTCTATCCGCTCATCTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 1380  
DB 422 TGCTTGAGCTTTTCTATPCCGTGTCTCTGCTGCTCTTCTATGTTCTTTGGAATGGCTTC 481  
QY 1381 AACTTTCATGATGATACAGCGACCGCGCGGCGGCACTGGAACCTGCTGATGTGACCATG 1440  
DB 482 AACTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541  
QY 1441 CTGTTTCTAGCCAGGAAATCCAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
DB 542 CTTTCTTGGCAATGAGTCTTACTCTGCTTTTATTTCTCAAGAAATGATGTCACGCTCAG 601  
QY 1501 CACTGCGCTTACCCAGGCAACTTCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
DB 602 CACTGCTCTGAAAAATCCCAATTTTGAATATGTCGCGCCACGCTTCTCTGACTGT 661  
QY 1561 CAT 1563

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Db 662 CGT 664

RESULT 6
BG529751
LOCUS
DEFINITION 602506022F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4698748 5',
mrna sequence.
ACCESSION BG529751
VERSION BG529751.1 GI:13521288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1529 row: k column: 05
High quality sequence stop: 764.
Location/Qualifiers
1. .840
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/db_xref="taxon:9606"
/clone="IMAGE:4698748"
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/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccattagccc); Site_2: SfiI (ggccattagccc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGCGGCCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 163 a 195 c 178 g 304 t
ORIGIN

Query Match 17.1%; Score 268; DB 12; Length 840;
Best Local Similarity 63.4%; Pred. No. 5.1e-52;
Matches 460; Conservative 0; Mismatches 260; Indels 6; Gaps 3;

Qy 811 TACCTCTACTTCCCTCTGCGCCACACTCATCTACAGGAGACTTACCCTAGGACGCC 870
Db 12 TATTGTGACTTCTTATGCTGCTTACCCTATCTACCGTGACAGCTATCCCAGGAATCCC 71

Qy 871 TATGTACAGTGAATATATGTGCGCAAGAACTTTGCCAGGCCCTGGGATGTGTGCTCAT 930
Db 72 ACTGTAAAGTGGGTATGTGCTATGAAGTTTGCACAGGCTTGTGTTTCTTCTAT 131

Qy 931 GCCTGCTTTCATCTGTGGCGCCCTGTGTCTTCTGTCTTTGCCAACATGAGCCGAGGCC 990
Db 132 GTGTACTACATCTTTGAAGGCTTTGTGCCCCCTTTGTTTCGGAATATCAACAGAGGCC 191

Qy 991 TTCAGCACCCGTGCGCTGCTCTCTATCTGTCATGCCAGTGTGCCAGGATCTTTCATG 1050
Db 192 TTCAGCGCTGCTGCTGCTCTATGTGTATTAACCTCTTCCAGGTGTGCTGAT 251

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Qy 1051 CTGCTGCTCA-TCTCTTTTGGCTTCTCCATTTGGCTCAACGCTTTGGCGAGATGCT 1109
Db 252 CTCTTCTTACTTTTGGCTTTCGCACTGCTGGCTCAATGCCTTTGTGAGATGTT 311

Qy 1110 ACGATTGGAGACAGAGATGTTCTACCGGAGCTGTGGAACTCAAGCTCTTCTCCAATA 1169
Db 312 ACGCTTTGGTGACAGATGTTCTATAAGGATTTGGTGAACCTCCAGCTCATACTCCAATA 371

Qy 1170 CTACCGCACTTTGGAACGCTGGTGGTCCATGAGTGGCTGTACAGCTACGTGTATCAGGATGG 1229
Db 372 TTATAGAACCTTGGATGTTGGTGGTCCATGAGTGGCTATATTACTATGTTTACAAGGACTT 431

Qy 1230 GCTCGGCTCTCTGCTGGTCCCGGCGGAGGTAGCCATGCTGGGTGTGTTCTGCTGCTC 1289
Db 432 TCTCTGGTCTTCTCCAGAGATTCAAATCTGCTGCCATGTTAGCTGTCTTTGCTGTATC 491

Qy 1290 CGCAGTGGCCCATGAGTATATCTTCTGCTGCTGCTGGGTTCTTCTATCCCGTCACTGCT 1349
Db 492 TCGTGTAGTACACGAATATGCTTGGCTGTTTGTGAGCTTTTCTATCCCGTCTCTT 551

Qy 1350 GATACTCTTCTCTGCTGAGGAGTCTTGAACCTTCATGATGATGATGATGATGATGATGATG 1408
Db 552 CGTGTCTTCTCATGTTCTTGTGAATGGCTTCAACTTCAATGATGATGATGATGATGATGATG 611

Qy 1409 GCCCGCATGGAAGCTGCTGATGTGGACCATGCTCTTTCTAGGCCAGGAA-----TCCAG 1464
Db 612 AGCCGATTGGAATGTTCTGATGTGGACTTCTCTTTCTTGGCAATGGAGTCTTACCT 671

Qy 1465 GTCAGCTGTACTGCGCAGGAGTGTGACGAGGCGGACTGCCCCCTTACCCAGGCAACT 1524
Db 672 CTGCTTTTATTCTCACGAAATGGTATGACGCTGACGCTGCTCTCTCTCTCTCTCTCTCTCT 731

Qy 1525 TTCTGG 1530
Db 732 TTTTGG 737

RESULT 7
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LOCUS AL527439 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC021YJ22 5
DEFINITION prime, mRNA sequence.
ACCESSION AL527439
VERSION AL527439.1 GI:12790932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 893)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .893
/organism="Homo sapiens"
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/clone="CS0DC021YJ22"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life

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182 TGGTGACAGGATGTTTATAAGGACTGGTGAACCTCTACATCATCTCCAACTACTACAG 241
QY 1176 CACTTGAACGCTGGTCCATGACTGGCTGACAGCTAGCTGATCAGGATGGCGCTCG 1235
Db 242 GACCTGGAACGCTGGTGGACGACTGGCTGCTACTACTATGTTTACAAAGACCTGCTCG 301
QY 1236 GCTCTTGGTGGCCGGCCGAGGGGTAGCCATGCTGGGTGTTCTCTGCTCCGCGAGT 1295
Db 302 GTTTTCTCGAAGAGGTTCAAACTCGCCGACATCTGCGCGTCTTCGCCCTGCGGCTGT 361
QY 1296 GGCCCATGATATATCTTCTGCTTCGTCGCGGGTCTTCTATCCCGCTCATGCTGACT 1355
Db 362 GGTGCACAGCTATCCCTGCGCATCTGCTGAGTACTTCTACCGGCTGCTTCTGCTGCT 421
QY 1356 CTTCTTGTCTATCGAGGAATGTTGAATCTCATGATCATGACGACGACGCGCCCGG 1415
Db 422 CTTCTATGTTCTTGAATGCTTAACTTCAATCTGTTTAACTGATGTTTAAAGAGGCAAT 481
QY 1416 ATGGAACGCTGCTGATGAGCACTGCTGTTTCTAGGCCAGGGAATCCAGGTACGCTGTA 1475
Db 482 CTCGAACATCACGCTTTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 1476 CTGCCAGAGTGTACGACGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1530
Db 542 GTCTCAAGAGTGGTATCGCCGACGACTGCTCATCTGAAGAAACCTACATTTCTGG 596

RESULT 9
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LOCUS 602659280F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802563 5',
DEFINITION mRNA sequence.
ACCESSION BG696168
VERSION BG696168.1 GI:13961039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10696 row: p column: 20
High quality sequence start: 5
High quality sequence stop: 738.
Location/Qualifiers
1. 741
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/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 140 a 160 c 163 g 278 t
ORIGIN
Query Match 15.6% Score 245; DB 12; Length 741;
Best Local Similarity 63.9%; Pred. No. 1.2e-46;
Matches 402; Conservative 0; Mismatches 225; Indels 2; Gaps 2;

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QY 902 TTGCCAGGCCCTGGGATGCTGCTATGCTCTATGCTCTGCTGCTGGCGGCTGCTGCTGCTTC 961
Db 13 TTGCACAGGCTCTTTGGTGTGCTTTTCTATGATGATGATGATGATGATGATGATGATGATG 71
QY 962 CTGTCTTTTGGCAACATGAGCGAGAGCCCTTTCAGACACCCGCTGCTGCTGCTGCTGCTGCT 1021
Db 72 CTTTGTTCGGAATATCAACACAGGAGCCCTTTCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
QY 1022 TGCATGCCAGCTTCCAGGAGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081
Db 132 TTAACCTCCATCTTCCAGGAGTGTGCTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 190
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Db 251 GGTGGAACCTCCAGCTCATCTACTTCCAACTATATAGAACCTGGAATGTTGGTGCTGCTGCT 310
QY 1202 GGCTGTACAGCTACGCTGATCAGGATGGGCTGCGGCTGCTTGGTCCCGGCGGCGGAGGG 1261
Db 311 GGCTATATGATGCTTACAGGAGCTTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 370
QY 1262 TAGCCATGCTGGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
Db 371 CTGCCATGTTAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
QY 1322 TCCTGGGGTCTTCTATCCCGCTCATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
Db 431 GCTTGGAGCTTTTCTATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
QY 1382 ACTTCATGATGCTGATGACGACGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1441
Db 491 ACTTCATGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
QY 1442 TGTTTCTAGGCGAGGATCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
Db 551 TTTTCTTGGGCAATGGAGCTTACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 610
QY 1502 ACTGCCCTTACCCCGACCACTTCTGCG 1530
Db 611 ACTGCTCTCTGAAAAATCCCACTTTTGG 639

RESULT 10
AI049480 731 bp mRNA linear EST 08-JUL-1998
LOCUS ub37ell.r1 Soares_thymus_2Nbmt Mus musculus cDNA clone
DEFINITION IMAGE:1379948 5' similar to gb:L21934 STEROL O-ACYLTRANSFERASE
(HUMAN); gb:L42293 Mus musculus acyl-coenzyme A:cholesterol
acyltransferase (MOUSE);, mRNA sequence.
ACCESSION AI049480
VERSION AI049480.1 GI:3297767
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 731)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

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[illegible]

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ACCESSION      AA867128.1  GI:2962573
VERSION
KEYWORDS
SOURCE
ORGANISM       Mus musculus
               house mouse.
REFERENCE
AUTHORS        Barra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
               Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
               Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
               Theising,B., Wylie,T., Lennon,G., Soares,B., Wilsson,R. and
               Waterston,R.
TITLE          The WashU-HMMI Mouse EST Project
JOURNAL        Unpublished (1996)
COMMENT        Contact: Marra M/Mouse EST Project
               WashU-HMMI Mouse EST Project
               Washington University School of MedicineP
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mouseest@watson.wustl.edu
               This clone is available royalty-free through LLNL ; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               MGI:667875
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 447.
               Location/Qualifiers
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               /strain="C57BL/6J"
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               /clone_lib="Soares_thymus_2NbMT"
               /sex="male"
               /tissue_type="Thymus"
               /dev_stage="4 weeks"
               /lab_host="DH10B"
               /note="Vector: p7T3D-Pac (Pharmacia) with a modified
               polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
               was primed with a Not I - oligo(dT) primer [5',
               TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGT
               3']; double-stranded cDNA was ligated to Eco RI adaptors
               (Pharmacia), digested with Not I and cloned into the Not I

```

and Eco RI sites of the modified pT7T3 vector. RNA

provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

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BASE COUNT      172 a   210 c   223 g   282 t
ORIGIN
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Best Local Similarity 64.1%; Pred. No. 5.2e-44;
Matches 352; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 1005 CCTGGTCTCTATCCTGATCCAGCTGTCAGGAGCTTCATGCTGCTCATCTT 1064
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QY 1065 CTTTGGCTTCTCATGCTGGCTCAACGCTTTCGGAGATCTAGGATTTGGAGACAG 1124
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Db 62 CTTTGGCTTCTTGGACGCTGGCTCAATGCTTTCGTGAGATTTAGCTTTGGTGACAG 121

QY 1125 GATGTTCTACGGGACGTGGTGAACCTCAACGCTCTTTCACAACTACTACGGCACTTGGAA 1184
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Db 122 GATGTTTATAAGGACGTGGTGAACCTTACATCATATCACTCAAGGACCTGGAA 181

QY 1185 CGTGGTGCTCAGTGGCTGTACAGCTACGCTATCATAGGATGGCTGGCTCTTGG 1244
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Db 182 CGTGGTGCTCAGTGGCTGTACTACTATGTTTACAAAGACTGCTCTGGTTTCTC 241

QY 1245 TGCCGGGGCCGAGGGTAGCCTGCTGGGTGTTTCTCGTCTCCGAGTGGCCCATGA 1304
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QY 1305 GTATATCTTCTGCTGCTGGGGTCTTCTATCCCGTCTGCTGATCTCTCTTGT 1364
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Db 542 CGGACTGG 550
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RESULT 14
AG133295
LOCUS      AG133295      635 bp      DNA      linear      GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-145020.F, genomic survey sequence.
ACCESSION AG133295
VERSION    AG133295.1 GI:16662973
KEYWORDS   GSS.
SOURCE     Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
ORGANISM   Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library PTB
JOURNAL    Unpublished
AUTHORS     2 (bases 1 to 635)
            Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
```

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimbases@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## PRIMERS

Sequencing: -21M13

## LIBRARY

Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
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/clone="PTB-145020.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT  
ORIGIN

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Query Match      14.5%; Score 227.6; DB 17; Length 635;
Best Local Similarity 90.6%; Pred. No. 1.3e-42;
Matches 259; Conservative 0; Mismatches 14; Indels 13; Gaps 1;

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QY 502 GTGACCTGGGTGCCAATGTTTCTGTCACCCCTGTTGGCCCGCTACAGGCCCTACGGCTG 561
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Db 207 GTGACCTGGGTGCCAATGTTTCTGTCACCCCTGTTGGCCCGCTACAGGCCCTGCGGATG 266

QY 562 TGGCCGAC-----GGGCACCTGGACGACGAGCGGGGCTGGGCTGTGCGCT 608
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 TGGCCGACGACGAGGGGCCAGAGCGCTCCGCGACGAGGTGACGGGCTGTGCTGTGCGCT 326

QY 609 TTTAGCCGCCACGCGCTGTGCTCTGCGCGCTGCGCGCTGCCAGTCCAGTGGCGTGGAGCATCA 668
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 GCTAGCGCCGCCACGCGCTGTGCTCTGCGCGCTGCGCGCTCCAGTCCAGTGGCGTGGAGCATCA 386

QY 669 GCTCCCGCGCGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
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Db 387 GCTCCCGCGCGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
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RESULT 15  
BG697784

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LOCUS      BG697784      848 bp      mRNA      linear      EST 07-MAY-2001
DEFINITION 602661272F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4804481 5',
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ACCESSION BG697784

VERSION BG697784.1 GI:13964385

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS NIH-MGC

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Search completed: April 30, 2003, 14:36:02  
Job time : 1619 secs

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GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 13:15:41 ; Search time 2498 Seconds  
(without alignments)  
15792.059 Million cell updates/sec

Title: US-09-918-026A-3

Perfect score: 1569

Sequence: 1 atggagccaggcgggccg.....cttggtctgcacacctag 1569

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | 1569   | 100.0         | 1569   | 34 | US-09-918-026A-3    |
| 3          | 1564.2 | 99.7          | 2040   | 24 | US-09-630-892-4     |
| 4          | 1564.2 | 99.7          | 2040   | 24 | US-09-630-892A-4    |
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| 8          | 1112.4 | 70.9          | 1607   | 17 | US-09-328-857A-1    |
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| 15         | 405.6  | 25.9          | 2129   | 1  | PCT-US02-21664-109  |
| 16         | 405.6  | 25.9          | 2729   | 41 | US-10-191-997-109   |
| 17         | 405.6  | 25.9          | 3499   | 18 | US-09-474-436-6552  |
| 18         | 405.6  | 25.9          | 3649   | 10 | US-08-657-621A-1    |
| 19         | 405.6  | 25.9          | 3688   | 23 | US-09-606-776-4846  |
| 20         | 405.6  | 25.9          | 3688   | 25 | US-09-644-873-10353 |
| 21         | 405.6  | 25.9          | 3688   | 25 | US-09-652-126-9964  |

22 405.6 25.9 3688 25 US-09-652-355-11001, A  
23 405.6 25.9 3688 25 US-09-652-911-10023  
24 405.6 25.9 3688 25 US-09-652-918-8702  
25 405.6 25.9 3688 26 US-09-663-693-1097  
26 405.6 25.9 3688 27 US-09-698-012-7756  
27 405.6 25.9 3688 27 US-09-699-998-10287  
28 405.6 25.9 3688 28 US-09-700-000-6981  
29 405.6 25.9 3688 29 US-09-726-174-4572  
30 405.6 25.9 3688 29 US-09-726-806-4704  
31 405.6 25.9 4011 9 US-08-509-187-3  
32 405.6 25.9 4011 9 US-08-509-187B-3  
33 405.6 25.9 4245 71 US-60-278-258-326  
34 405.6 25.9 4245 76 US-60-324-185-12727  
35 403.6 25.7 418 16 US-09-235-076-33158  
36 403.6 25.7 418 16 US-09-277-227-3194  
37 403.6 25.7 418 17 US-09-332-782-33158  
38 403.6 25.7 418 29 US-09-737-223-33158  
39 403.6 25.7 418 34 US-09-909-627-3194  
40 403.6 25.7 418 34 US-09-918-995-33158  
41 399.8 25.5 3649 10 US-08-657-620A-1  
42 394.8 25.2 4846 61 US-60-172-373-859  
43 391 24.9 399 16 US-09-235-076-33281  
44 391 24.9 399 16 US-09-277-227-3079  
45 391 24.9 399 17 US-09-332-782-33281

ALIGNMENTS

RESULT 1  
PCT-US02-22746-3  
; Sequence 3, Application PC/TUS0222746  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Rosanne M. Crooke  
; APPLICANT: Mark J. Graham  
; APPLICANT: Kristina M. Lomonidis  
; TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL ACYLTRANSFERASE-2  
; FILE OF INVENTION: EXPRESSION  
; FILE REFERENCE: ISPH-0694  
; CURRENT APPLICATION NUMBER: PCT/US02/22746  
; CURRENT FILING DATE: 2002-07-15  
; PRIOR APPLICATION NUMBER: 09/918,026  
; PRIOR FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 65  
; SEQ ID NO 3  
; LENGTH: 1569  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1569)  
PCT-US02-22746-3

Query Match 100.08; Score 1569; DB 1; Length 1569;  
Best Local Similarity 100.08; Pred. No. 0;  
Matches 1569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCCAGGCGGCGCCGCTGCGCTGTCAGAGGACAGAGGCGTGGAGGGAGCGG 60  
Db 1 ATGGAGCCAGGCGGCGCCGCTGCGCTGTCAGAGGACAGAGGCGTGGAGGGAGCGG 60

QY 61 GAGCGCCAAACCCTGTGGAGATGGAACACTGAGAGCGACAGAGCCCGGACTTGTACAA 120  
Db 61 GAGCGCCAAACCCTGTGGAGATGGAACACTGAGAGCGACAGAGCCCGGACTTGTACAA 120

QY 121 TGAGCCGACACATGAGGCTGTGAGGACACATTCCTGGAGCAAGCGGAGGACAACTG 180  
Db 121 TGAGCCGACACATGAGGCTGTGAGGACACATTCCTGGAGCAAGCGGAGGACAACTG 180

QY 181 AGGAGCTGCTGAGTGGGCGCATCGGGAGGCTATACAACTCTACCATCACAAGACAAA 240  
Db 181 AGGAGCTGCTGAGTGGGCGCATCGGGAGGCTATACAACTCTACCATCACAAGACAAA 240

QY 241 CCTCTGCCCCACCTCCCCAGGTTCTTTGAGCAGGACCCAGGAGCCATCCCTGGGAAA 300  
Db 241 CCTCTGCCCCACCTCCCCAGGTTCTTTGAGCAGGACCCAGGAGCCATCCCTGGGAAA 300

QY 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGAGCATTTTC 360  
Db 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGAGCATTTTC 360

QY 361 CGCACCATTACACATGTTTCATCCTGCGCTGCTGCTTTCATCATCAGCACCCTGGCC 420  
Db 361 CGCACCATTACACATGTTTCATCCTGCGCTGCTGCTTTCATCATCAGCACCCTGGCC 420

QY 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTACGTTTC 480  
Db 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTACTGATCTTACGTTTC 480

QY 481 GGACAGCTGCCATTGGCGTGTGAGCTGGTGGTGGCCATGTTTCTGCCACCCTGTTGGG 540  
Db 481 GGACAGCTGCCATTGGCGTGTGAGCTGGTGGTGGCCATGTTTCTGCCACCCTGTTGGG 540

QY 541 CGGTACAGGCGCTACGCGTGTGGGCGAGGGCACCTGGAGCGAGCGGCGCTGGGC 600  
Db 541 CGGTACAGGCGCTACGCGTGTGGGCGAGGGCACCTGGAGCGAGCGGCGCTGGGC 600

QY 601 TGTGCGCTTTTAGCGCCGCCACGCGTGTGCTGCTGCGCGCTGCCGTCACAGTGGCCGTG 660  
Db 601 TGTGCGCTTTTAGCGCCGCCACGCGTGTGCTGCTGCGCGCTGCCGTCACAGTGGCCGTG 660

QY 661 GAGCATCAGCTCCCGCGGCTCCCGTTGTCTCTGCTTTCGAGCAGGTTAGGTTCTCTG 720  
Db 661 GAGCATCAGCTCCCGCGGCTCCCGTTGTCTCTGCTTTCGAGCAGGTTAGGTTCTCTG 720

QY 721 ATGAAAAGCTTACTCTTCTGAGAGAGGCTGTCCTGGGATCCTTCGTGCCAGACAGGT 780  
Db 721 ATGAAAAGCTTACTCTTCTGAGAGAGGCTGTCCTGGGATCCTTCGTGCCAGACAGGT 780

QY 781 GAGGGATCCAGGCGCCCGCTTCTCCAGCTACTCTTCTGCTTCTTCTGCCAACACTC 840  
Db 781 GAGGGATCCAGGCGCCCGCTTCTCCAGCTACTCTTCTGCTTCTTCTGCCAACACTC 840

QY 841 ATCTACAGGAGACTTACCCTAGGACGCCCTATGTCAGTGGAAATATGTGGCAGAAC 900  
Db 841 ATCTACAGGAGACTTACCCTAGGACGCCCTATGTCAGTGGAAATATGTGGCAGAAC 900

QY 901 TTGCGCCAGGCGCTGGGATGTGCTCTATGCTGCTTCTGCTGCGCCGCTCTGTGTT 960  
Db 901 TTGCGCCAGGCGCTGGGATGTGCTCTATGCTGCTTCTGCTGCGCCGCTCTGTGTT 960

QY 961 CCTGCTTTTGCCAAACATGAGCGGAGAGCCCTTACGACCCGCTGCTGCTCTATC 1020  
Db 961 CCTGCTTTTGCCAAACATGAGCGGAGAGCCCTTACGACCCGCTGCTGCTCTATC 1020

QY 1021 CTGATGCCAGGTTGCCAGGCACTTTCATGCTGCTGCTCTCTTCTTCTGCTTCTCCAT 1080  
Db 1021 CTGATGCCAGGTTGCCAGGCACTTTCATGCTGCTGCTCTCTTCTTCTGCTTCTCCAT 1080

QY 1081 TGCTGGCTCAACGCTTTGCCGAGATGCTAGATTGGAGACAGGATGTTCTACCGGGAC 1140  
Db 1081 TGCTGGCTCAACGCTTTGCCGAGATGCTAGATTGGAGACAGGATGTTCTACCGGGAC 1140

QY 1141 TGGTGGAACTCAAGCTCCTTCTCCAACCTACTACCGCACTTGGAAACGTTGGTGGTCCATGAC 1200  
Db 1141 TGGTGGAACTCAAGCTCCTTCTCCAACCTACTACCGCACTTGGAAACGTTGGTGGTCCATGAC 1200

QY 1201 TGGCTGTACAGTACGTGTATCAGATGGGCTGGGCTTCTTGGTGGCCGCGCGAGGG 1260  
Db 1201 TGGCTGTACAGTACGTGTATCAGATGGGCTGGGCTTCTTGGTGGCCGCGCGAGGG 1260

QY 1261 GTAGCCATGCTGGTGTGTTCTGCTCCGAGTGGCCCATGATATATCTTCTGCTTC 1320  
Db 1261 GTAGCCATGCTGGTGTGTTCTGCTCCGAGTGGCCCATGATATATCTTCTGCTTC 1320



Qy 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGGTGACACTCGATCTTGCTCTGC 1560  
Db 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGGTGACACTCGATCTTGCTCTGC 1560  
Qy 1561 CATACCTAG 1569  
Db 1561 CATACCTAG 1569

RESULT 3  
US-09-630-892-4  
; Sequence 4, Application US/09630892  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.  
; APPLICANT: Oelkers, Peter  
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL  
; TITLE OF INVENTION: ACYLTRANSFERASE  
; FILE REFERENCE: 0575/56331-A  
; CURRENT APPLICATION NUMBER: US/09/630.892  
; CURRENT FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Yeast  
US-09-630-892-4

Query Match 99.7%; Score 1564.2; DB 24; Length 2040;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAGCCAGGCGGCGCGCTGCTGCTGAGAGGACAGAGGCTGGAGGGGAGCGG 60  
; Db 52 ATGGAGCCAGGCGGCGCGCTGCTGCTGAGAGGACAGAGGCTGGAGGGGAGCGG 111  
Qy 61 GAGCGCAACCCCTGTGGAGTGGAAACACTGAGACGACAGAGCGCCCGGACTTGTGACAA 120  
; Db 112 GAGCGCAACCCCTGTGGAGTGGAAACACTGAGACGACAGAGCGCCCGGACTTGTGACAA 171  
Qy 121 TGGACCCGACATGAGGCTGTGAAGCACAATGCTGGAGCAGCGACGAGCAACTG 180  
; Db 172 TGGACCCGACATGAGGCTGTGAAGCACAATGCTGGAGCAGCGACGAGCAACTG 231  
Qy 181 AGGAGCTGCTGATCGGCGCCATGGGAGGCTATACATCTACCCATCAACAGACAAA 240  
; Db 232 AGGAGCTGCTGATCGGCGCCATGGGAGGCTATACATCTACCCATCAACAGACAAA 291  
Qy 241 CTTCTGCCCCACCTCCCGGCTTCTTGGAGCAGGACCCAGGAGCCATCCCTGGGAAA 300  
; Db 292 CTTCTGCCCCACCTCCCGGCTTCTTGGAGCAGGACCCAGGAGCCATCCCTGGGAAA 351  
Qy 301 CAGAAAGTTTTCATCATCGCAAGTCCCTGCTGTATGAGCTGATGAGGTGACGATTTTC 360  
; Db 352 CAGAAAGTTTTCATCATCGCAAGTCCCTGCTGTATGAGCTGATGAGGTGACGATTTTC 411  
Qy 361 CGCACCATCTACACATGTTTCATCGCTGCGCTGTGTGCTTTCATCATGACACCCCTGGCC 420  
; Db 412 CGCACCATCTACACATGTTTCATCGCTGCGCTGTGTGCTTTCATCATGACACCCCTGGCC 471  
Qy 421 ATGACTTTCATGATGAGGCGAGGCTGCTGGAGTTTGACCTACTGATCTTACGCTTC 480  
; Db 472 ATGACTTTCATGATGAGGCGAGGCTGCTGGAGTTTGACCTACTGATCTTACGCTTC 531  
Qy 481 GGACAGCTGCATTTGGCGCTGGTGAGCTGGTGCCCATGTTTCTGCCACCCCTGTTGGCG 540  
; Db 532 GGACAGCTGCATTTGGCGCTGGTGAGCTGGTGCCCATGTTTCTGCCACCCCTGTTGGCG 591  
Qy 541 CCGTACAGGCCCTTACGGCTGTGGGCGAGGGGACCTTGACGAGCGGAGCGGCGCTGGGC 600  
; Db 592 CCGTACAGGCCCTTACGGCTGTGGGCGAGGGGACCTTGACGAGCGGAGCGGCGCTGGGC 651  
Qy 601 TGTGCGGCTTTTAGCGCGCCACGCGGTGGTGCTCTGCGCGCTGCGCGGTCCACGCTGGCGCTG 660

RESULT 4  
US-09-630-892A-4  
; Sequence 4, Application US/09630892A  
; GENERAL INFORMATION:  
; APPLICANT: Sturley, Stephen L.

Db 652 TGTGGCGCTGCTAGCGGCCACCGCGTGGTGTCTGCGGGCTGCGGTCCAGGTGGCCGTG 711  
Qy 661 GAGCATCAGTCCCGCGCGCTCCCGTGGTGTCTTCCAGCAGGTAGTGTCTG 720  
Db 712 GAGCATCAGTCCCGCGCGCTCCCGTGGTGTCTTCCAGCAGGTAGTGTCTG 771  
Qy 721 ATGAAAGCTACTCTTCTGAGAGAGGCTGCTGGGATCCTTCTGCGCAGAGAGGT 780  
Db 772 ATGAAAGCTACTCTTCTGAGAGAGGCTGCTGGGATCCTTCTGCGCAGAGAGGT 831  
Qy 781 GAGGGATCCAGGCCCGCGAGTTTCTCCAGTACCTTCTACTTCTCTCTGCGCCACACTC 840  
Db 832 GAGGGATCCAGGCCCGCGAGTTTCTCCAGTACCTTCTACTTCTCTCTGCGCCACACTC 891  
Qy 841 ATCTACAGGAGACTTACCCTTAGGCGCCCTATGTCAGTGGAAATATGTGCCAAGAAC 900  
Db 892 ATCTACAGGAGACTTACCCTTAGGCGCCCTATGTCAGTGGAAATATGTGCCAAGAAC 951  
Qy 901 TTTGCCAGGCCCTGGGATGTGTCTATGCTGCTCATCTCTGGGCGCGCTCTGTGT 960  
Db 952 TTTGCCAGGCCCTGGGATGTGTCTATGCTGCTCATCTGCGCGCGCTCTGTGT 1011  
Qy 961 CTTGTCTTTGCCAACAATGAGCGGAGAGCGCTTCCAGCACCGTGGCTGTCTCTATC 1020  
Db 1012 CTTGTCTTTGCCAACAATGAGCGGAGAGCGCTTCCAGCACCGTGGCTGTCTCTATC 1071  
Qy 1021 CTGCATGCCACGTTGGCAGGATCTTCTATGCTGCTCATCTTCTTGGCTTCTCTCAT 1080  
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Qy 1081 TGCTGGCTCAACGCCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAC 1140  
Db 1132 TGCTGGCTCAACGCCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAC 1191  
Qy 1141 TGTGGAACTCAACGCTCTTCTCCAACTACTACCGCACTTGGAACTGGTGGTCCATGAC 1200  
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Qy 1201 TGGCTGTACAGCTACGCTGTATCAGGATGGGCTGCGGCTCCTTGGTGGCGGCGCGG 1260  
Db 1252 TGGCTGTACAGCTACGCTGTATCAGGATGGGCTGCGGCTCCTTGGTGGCGGCGCGG 1311  
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Db 1312 GTAGCCATGCTGGGTGTTCTTCTGCTCGCAGTGGCCCATGAGTATATCTTCTGCTTC 1371  
Qy 1321 GTCCTGGGGTTCTTCTATCCCGTCATCTGATCTTCTTCTGCTGAGGAAATGTTG 1380  
Db 1372 GTCCTGGGGTTCTTCTATCCCGTCATCTGATCTTCTTCTGCTGAGGAAATGTTG 1431  
Qy 1381 AACTTCATGATGATGACCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440  
Db 1432 AACTTCATGATGATGACCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1491  
Qy 1441 CTGTTCTTAGCGCAGGGAATCCAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1500  
Db 1492 CTGTTCTTAGCGCAGGGAATCCAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1551  
Qy 1501 CACTGCCCGTTTACCCAGGCAACTTTCTGGGGCTGGTGACACCTCGATCTTGTCTCTGC 1560  
Db 1552 CACTGCCCGTTTACCCAGGCAACTTTCTGGGGCTGGTGACACCTCGATCTTGTCTCTGC 1611  
Qy 1561 CATACCTAG 1569  
Db 1612 CATACCTAG 1620



APPLICANT: Oelkers, Peter  
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL  
; FILE REFERENCE: 0575/56331-A  
; CURRENT APPLICATION NUMBER: US/09/630,892A  
; CURRENT FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: yeast  
US-09-630-892A-4

Query Match 99.7%; Score 1564.2; DB 24; Length 2040;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGGAGCCAGCGGGCCCGCTGCTGCTGTCAGAGGACAGAAAGGCTGGGAGGGAGCGG 60  
DB 52 ATGGAGCCAGCGGGCCCGCTGCTGCTGTCAGAGGACAGAAAGGCTGGGAGGGAGCGG 111  
QY 61 GAGCCCAACCTGTGGAGATGGAACACTGAGAGCGACAGAGCCCGGACTTGTACAA 120  
DB 112 GAGCCCAACCTGTGGAGATGGAACACTGAGAGCGACAGAGCCCGGACTTGTACAA 171  
QY 121 TGAACCCGACACATGAGGCTGTGAAGGCACAAATGCTGGAGCAAGCGCAGGACAACTG 180  
DB 172 TGAACCCGACACATGAGGCTGTGAAGGCACAAATGCTGGAGCAAGCGCAGGACAACTG 231  
QY 181 AGGAGCTGCTGGATCGGGCCATGCGGAGGCTATACAAATCCATCCATCAAGACAAA 240  
DB 232 AGGAGCTGCTGGATCGGGCCATGCGGAGGCTATACAAATCCATCCATCAAGACAAA 291  
QY 241 CCTCTGCCCCACCTCCCGGAGTTCCTTGACAGAGCCAGAGGCCATCCCTGGGAAA 300  
DB 292 CCTCTGCCCCACCTCCCGGAGTTCCTTGACAGAGCCAGAGGCCATCCCTGGGAAA 351  
QY 301 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGAGGATTTTC 360  
DB 352 CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGAGGTGAGGATTTTC 411  
QY 361 CGCACCATCTACCAATGTTCAATCGCTGCGCTGTGTCTTTCATCATCAGCACCCTGGCC 420  
DB 412 CGCACCATCTACCAATGTTCAATCGCTGCGCTGTGTCTTTCATCATCAGCACCCTGGCC 471  
QY 421 ATCGACTTCATGATGAGGCGAGGCTGCTGCTGAGTGTGACCTACTGATCTTCAGCTTC 480  
DB 472 ATCGACTTCATGATGAGGCGAGGCTGCTGCTGAGTGTGACCTACTGATCTTCAGCTTC 531  
QY 481 GGACAGCTGCCATTTGGCGCTGTGACCTGGGTGCCCATGTTTCTGTCCACCCCTGTTGGG 540  
DB 532 GGACAGCTGCCATTTGGCGCTGTGACCTGGGTGCCCATGTTTCTGTCCACCCCTGTTGGG 591  
QY 541 CCGTACCAAGCCCTAGGCTGTGGCCAGGGGCGACCTGGACGCGAGCGGCGCTGGGC 600  
DB 592 CCGTACCAAGCCCTAGGCTGTGGCCAGGGGCGACCTGGACGCGAGCGGCGCTGGGC 651  
QY 601 TGTGGCGCTTTTAGCGCCGACACCGCTGTGTGCTCTGCGCGCTCCGCTGACCGTGGCCG 660  
DB 652 TGTGGCGCTTTTAGCGCCGACACCGCTGTGTGCTCTGCGCGCTCCGCTGACCGTGGCCG 711  
QY 661 GAGCATCAGCTCCCGCGCCCTCCGCTGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB 712 GAGCATCAGCTCCCGCGCCCTCCGCTGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 771  
QY 721 ATGAAAGCTACTCTCTCTGAGAGGCTGTGCTGGATCTTCTGCTGCTGCTGCTGCTGCT 780  
DB 772 ATGAAAGCTACTCTCTCTGAGAGGCTGTGCTGGACCTCTTCTGCTGCTGCTGCTGCTGCT 831  
QY 781 GAGGGATCCAGGCGCCCGGCTTCTCCAGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840  
DB 832 GAGGGATCCAGGCGCCCGGCTTCTCCAGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 891

QY 841 ATCTACAGGAGACTTACCTTAGGAGCGCCTATGTCAGGTGGAATTTATGTGGCAAGAAC 900  
DB 892 ATCTACAGGAGACTTACCTTAGGAGCGCCTATGTCAGGTGGAATTTATGTGGCAAGAAC 951  
QY 901 TTTGCCAGGCGCTGGGATGTGTCTATGCTGCTTATGCTTCCATCTGGGCGCCTCTGTGT 960  
DB 952 TTTGCCAGGCGCTGGGATGTGTCTATGCTGCTTATGCTTCCATCTGGGCGCCTCTGTGT 1011  
QY 961 CCTGTCTTTGCCAACATGAGCGGAGAGCGCTTTCAGGACCGGCTGCGCTGTCTCTATC 1020  
DB 1012 CCTGTCTTTGCCAACATGAGCGGAGAGCGCTTTCAGGACCGGCTGCGCTGTCTCTATC 1071  
QY 1021 CTGCATGCCACCTTCCAGGCACTTCTATGCTGCTGCTCATCTTCTTTGCCCTTCCCTCAT 1080  
DB 1072 CTGCATGCCACCTTCCAGGCACTTCTATGCTGCTGCTCATCTTCTTTGCCCTTCCCTCAT 1131  
QY 1081 TCGTGGCTCAACGCTTTCCGAGATGCTTACGATTTGGAGAGAGGATGTTTACCGGGAC 1140  
DB 1132 TCGTGGCTCAACGCTTTCCGAGATGCTTACGATTTGGAGAGAGGATGTTTACCGGGAC 1191  
QY 1141 TGGTGGAACTCAACGCTTCTCCAACTACTACCGCACTTGGAACTGCTGTGCTCCATGAC 1200  
DB 1192 TGGTGGAACTCAACGCTTCTCCAACTACTACCGCACTTGGAACTGCTGTGCTCCATGAC 1251  
QY 1201 TGGCTGTACAGCTACGCTGTATCAGGATGGGCTGCGGCTCCTTTGGTCCCGGCGCGAGGG 1260  
DB 1252 TGGCTGTACAGCTACGCTGTATCAGGATGGGCTGCGGCTCCTTTGGTCCCGGCGCGAGGG 1311  
QY 1261 GTAAGCATGCTGGGTGTGTCTGCTCCGAGTGGGCCCATGATATATCTTCTGCTTC 1320  
DB 1312 GTAAGCATGCTGGGTGTGTCTGCTCCGAGTGGGCCCATGATATATCTTCTGCTTC 1371  
QY 1321 GTCTGGGGTCTTCTATCCCGTCACTGCTGATCTTCTTGTGCTATTTGGAGGAATGTTG 1380  
DB 1372 GTCTGGGGTCTTCTATCCCGTCACTGCTGATCTTCTTGTGCTATTTGGAGGAATGTTG 1431  
QY 1381 AACTTCATGATCATGACAGGCGACCGCGCGGCTGGAAGCTGCTGATGTGGACCATG 1440  
DB 1432 AACTTCATGATCATGACAGGCGACCGCGCGGCTGGAAGCTGCTGATGTGGACCATG 1491  
QY 1441 CTGTTTCTAGGCGAGGAAATCCAGGTCAGCTGCTACTGCGAGGATGTTGACGACGCGG 1500  
DB 1492 CTGTTTCTAGGCGAGGAAATCCAGGTCAGCTGCTACTGCGAGGATGTTGACGACGCGG 1551  
QY 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGCTGACACCTCGATCTTGGTCTCTGC 1560  
DB 1552 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGCTGACACCTCGATCTTGGTCTCTGC 1611  
QY 1561 CATACCTAG 1569  
DB 1612 CATACCTAG 1620

RESULT 5  
US-09-328-857A-2  
; Sequence 2, Application US/09328857A  
; GENERAL INFORMATION:  
; APPLICANT: Cases, Sylvaine  
; APPLICANT: Farese, Robert  
; APPLICANT: Novak, Sabine  
; APPLICANT: Erickson, Sandra  
; TITLE OF INVENTION: Novel Acyl CoA:Cholesterol Acyl  
; FILE REFERENCE: 6510-104US1  
; CURRENT APPLICATION NUMBER: US/09/328,857A  
; CURRENT FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: 60/090,354  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1509







QY 325 TCCCTGCTTGATGAGTGCAGGATTTCCGACCAATCTACACATGTTTCATC 384  
Db 351 TCATGATCGATGAGCTAATGGAGTGCAACATTTCCGAACCATCTACACATGTTTCATA 410  
QY 385 GCTGCCCTGTGTCTTCATCATCAGACACCTGGCCATCGAGCTTCATTGATGAGGGCAGG 444  
Db 411 GCGGGCCTATGGTCTTGATCATCAGCACCCCTGGCCATCGAGCTTCATTGATGAGGGCAGG 470  
QY 445 CTGCTGCTGGAGTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTG 504  
Db -471 TTGATGCTGGAGTTGACTTACTCTCTTCAGCTTCGGACAGCTGCCCTTGGCGCTGATG 530  
QY 505 ACCTGGGTGCCATGTTCTTCFCCACCCTGTGGCGCGCTACCGGCCCTACCGGTGTGG 564  
Db 531 ACCTGGGTGCCATGTTCTCTGATATACGCTTCCTAGTGGCCCTACCGACCCCTGTGGCTGG 590  
QY 565 GCCA-----GGGGACCTTGGAGCGAGCGAGCGCGCTGGCTGTGCGCTTTTA 612  
Db 591 GCCAGCGCGGGTGGGGGTGCGTGATGCTGGGGGCGAGCTGGGCTGCGCTTCTGCTG 650  
QY 613 GCGGCCACCGCGTGTCTGCGCGGTGCGCGGTCCACGTGCGCGTGGAGCATCAGCTC 672  
Db 651 GCTGCCACCGTGTGCTGCTGCTGCTGCTGCGCGGTGCGAGTGTGAGTGAGGCTGAGCTT 710  
QY 673 CCGCGCGCTCCCGTGTGCTGCTGCTGCTGCTGAGCAGGTTAGTTCCTGATGAAAAGCTAC 732  
Db 711 CCGCGCGCTCGCGTGTGCTGCTGCTGCTGAGCAGGTCAGATTGCTGATGAAAAGCTAC 770  
QY 733 TCCCTTCCTGAGAGAGGCTGTGCTGGGATCCTTCGTGCCAGAGAGGTCAGGGGATCCAG 792  
Db 771 TCCCTTCCTGAGAGAGCTGTGCTGGGATCCTTTTGTGACAGAGGAAAGGCGATCAGC 830  
QY 793 GCCCCAGTTTCTCCAGCTACCTCTACTTCTCTCTGCCCCAACACTCATCTACAGGGAG 852  
Db 831 CCCCCAAGTTTCTCCAGCTACCTCTACTTCTCTCTGCCCCAACACTCATCTACAGAGAG 890  
QY 853 ACTTACCCTAGGACGCCCTATGTCAGGTGGAATATGTGGCCAAAGAACTTTGCCCAGGCC 912  
Db 891 ACATACCCAGGACACCCAGCATCAGGTGGAATATGTGGCCAAAGAACTTTGCCCAGGTC 950  
QY 913 CTGGGATGTGCTATGCTGCTATGCTCTATCTCTGCGCGCGCTGTGTTCTCTCTTGGC 972  
Db 951 CTGGGCTGTGCTCTATGCTGCTTCTATCTCTGCGCGCGCTGTGTTCTCTCTTGGC 1010  
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Db 1011 AACATGAGCGGGAACCCCTTCAGCACCCGCGCTGCTCTCTCTATCTGATGCCAGG 1070  
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Db 1131 GCCTTTGGCGAGATGCTGCGGTTTGGAGACAGGATGTTCTACCGGAGCTGTGGAACTCG 1190  
QY 1153 AGCTCTCTTCCAACTACTACCGCACTTTGGAACGTTGGTGGTCCATGACTGGCTGTACAGC 1212  
Db 1191 ACTTCTCTTCCAACTACTACCGCACTTGGAACTGTTGGTGGTCCATGACTGGCTGTACAGC 1250  
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Db 1251 TAGCTGTATCAAGATGGGTGTGGCTCTTAGGACAGCGCGGCTGCGGGGTGCCATGCTG 1310  
QY 1273 GGTGTGTTCTGCTCCGACGTGGCCATGATATATCTCTGCTGCTGCTGCTGCGGTTTC 1332  
Db 1311 GGAGTGTTCCTGGTGTCTGCGGTGGTTTATGAGTATATCTCTGCTGCTGCTGCGGTTTC 1370  
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Db 1371 TTCTACCCCGGTGATGCTGATGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1430  
QY 1393 CATGACACGCGCACCGGCCCGGATGGAACGCTGCTGATGGAACCATGCTGTTCTTAGGC 1452

Db 1431 AACGACAGGCACACAGGTCAGCTCCAGCTGGAACATCTCTGATGACCTTTCTCTTCATGGGC 1490  
QY 1453 CAGGAATCCAGGTCAGCTGTACTGCCAGGAGTGGTAGCAGCGGGGACACTGCCCTTA 1512  
Db 1491 CAGGCGATCCAGGTCAGCTGTACTGCCAGGAGTGGTAGCTCGTCGACAGACTGTCCCTG 1550  
QY 1513 CCCCAGGCAACTTCTGGGGCTGGTGACACCTTCGATCTTGGTCTTCCCATACCTAG 1569  
Db 1551 CCCCAGACAACTTCTGGGGATGGTGACACCCCAATCTTGGTCTTCCCATACCTAG 1607

RESULT 9  
US-09-918-026A-10  
; Sequence 10, Application US/09918026A  
; GENERAL INFORMATION:  
; APPLICANT: Rosanne M. Crooke  
; APPLICANT: Mark J. Graham  
; TITLE OF INVENTION: Antisense Modulation of Acyl CoA Cholesterol Acyltransferase-2  
; FILE REFERENCE: ISPH-0588  
; CURRENT APPLICATION NUMBER: US/09/918,026A  
; CURRENT FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 65  
; SEQ ID NO 10  
; LENGTH: 1607  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)...(1607)  
; NAME/KEY: unsure  
; LOCATION: (176)  
; OTHER INFORMATION: a, c, g or t  
US-09-918-026A-10

Query Match 70.9%; Score 1112.4; DB 34; Length 1607;  
Best Local Similarity 83.2%; Pred. No. 1.4e-237;  
Matches 1295; Conservative 0; Mismatches 247; Indels 15; Gaps 2;

QY 28 CTGCAGAGCACAGAGGGCTGGAGGGAGCGGGAGCGCCCAACCCCTGT---GGAGATGA 84  
Db 51 CTTGGAGGAGAGAGAGGGCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 110  
QY 85 AACATGAGCACACAGAGCCCGGACTTGGTACATGACCGACACATGAGAGGCTGTG 144  
Db 111 AACGCAAGCACACAGGAAACCCAGACTTGGTGCAATGACTCGACATATGAGGCTGTG 170  
QY 145 AAGGCACAATTCGTGGAGCAAGCGGAGGAGCAACTGAGGAGGCTGCTGGATCGGGCCATG 204  
Db 171 AAGACNCACTTCTGGAGCAAGCACAGAGAGAGTGGCAGAGCTGTGGATCGGGCCCTA 230  
QY 205 CCGGAGGCTATACAATCTACCCATCACAAAGACAAACCTCTGCCCCACCTCCGCCAGGT 264  
Db 231 TGGAGGCTATGCAAGCTTACCCCAAAAGACAGACACTTCTCCCTCCGCTGCCCCAGAT 290  
QY 265 TCCTTTGAGCAGGACCCAGGAGCCATCCCTGGGAAACAGAAAAGTTTTCATCTATCCGCAAG 324  
Db 291 TCTACAAGCAAGAACCCCGGAGTTACGCCCTTGGAAAACGGAAGTTTTCGTCGCCGCCAAG 350  
QY 325 TCCTGCTGTGATGAGCTGTATGAGGTCAGAGCTTCGGCACCATCTACACATGTTTCATC 384  
Db 351 TCACCTGATCGATGAGCTAATGAGGTCGAACATTTCCGAACCATCTACACATGTTTCATA 410  
QY 385 GCTGGCCTGTGCTCTTTCATCATCAGCACCCCTGGCCATGACCTTCATGATGAGGCGAGG 444  
Db 411 GCGGGCTATGGTCTTGTGATCATCAGCACCCCTGGCCATGACCTTCATGATGAGGCGAGG 470  
QY 445 CTGCTGCTGGAGTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGGTG 504  
Db 471 TTGATGCTGGAGTTGACCTACTCTCTCAGCTTCGGACAGCTGCCCTTGGCGCTGATG 530  
QY 505 ACCTGGGTGCCCATGTTTCTGTCACCCCTGTGGCGCGCGTTACGAGGCCCTACGGCTGTGG 564

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Db 531 ACCTGGTTCCCATGTTCTCTGTATAGCTCCTAGTCCCTACCAGACCTCTGGCTGTGG 590
Qy 565 GCCA-----GGGCACTTGGACGACGACGGCGCTGGCTGTGGCTTTTA 612
Db 591 GCCAGCCGCGCTGGGGTCTGGATGCTGGGGCCAGCTGGCTGCTTCTGCTG 650
Qy 613 GCGCCACCGCTGTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 672
Db 651 GCTGCCACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
Qy 673 CCGCGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Db 711 CCGCGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 770
Qy 733 TCCCTCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
Db 771 TCCCTCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
Qy 793 GCGCCAGTTCTCCAGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852
Db 831 CCGCCAGTTCTCCAGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 890
Qy 853 ACTTACCCTAGGACGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912
Db 891 ACATACCCAGGACACCCAGCATCAGGTGGAATATGCTGCTGCTGCTGCTGCTGCTG 950
Qy 913 CTGGGATGTGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 972
Db 951 CTGGGCTGTTGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010
Qy 973 AACATGACGAGAGGCTTCCAGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
Db 1011 AACATGACGAGAGGCTTCCAGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070
Qy 1033 TTGCCAGCATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
Db 1071 GGGCCAGCATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
Qy 1093 GCTTTGCGGAGATGCTACGATTTGGACAGGATGTTCTACCGGGAGCTGGTGAAC 1152
Db 1131 GCTTTGCGGAGATGCTGGGTTGGACAGGATGTTCTACCGGGAGCTGGTGAAC 1190
Qy 1153 AGCTCCTTCTCAACTACTACGCACTTGGACAGGCTGCTGCTGCTGCTGCTGCTGCT 1212
Db 1191 ACTTCTCTTCCAACTACTACGCACTTGGACAGGCTGCTGCTGCTGCTGCTGCTGCT 1250
Qy 1213 TACGCTATCAGGATGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
Db 1251 TATGCTATCAGATGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1310
Qy 1273 GGTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
Db 1311 GGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1370
Qy 1333 TTCTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1392
Db 1371 TTCTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1430
Qy 1393 CATGACGAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1452
Db 1431 AAGCAGGACACAGGCTCCAGCTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCT 1490
Qy 1453 CAGGGAATCCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1512
Db 1491 CAGGCAATCCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1550
Qy 1513 CCGCAGCAACTTCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1569
Db 1551 CCGCAGCAACTTCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1607
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US-60-229-512-505
; Sequence 505, Application US/60229512
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHASE II
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000770
; CURRENT APPLICATION NUMBER: US/60/229,512
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 505
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: HUMAN
US-60-229-512-505
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Query Match 34.7%; Score 544.8; DB 66; Length 2154;
Best Local Similarity 65.8%; Pred. No. 6.3e-111;
Matches 878; Conservative 0; Mismatches 357; Indels 99; Gaps 2;

Qy 189 GCTGGATCGGGCATCGGGAGGCTATACATCTTACCCATCACAAGACAAACCTCTG 248
Db 541 GCTGGATCGGGCATCGGGAGGCTATACATCTTACCCATCACAAGACAAACCTCTG 600
Qy 249 CCCACCTCCCGAGGTTCTTGAGCAGGACCCAGGAGCCATCCCTGGGGAACAAAGT 308
Db 601 CCCACCTCCCGAGGTTCTTGAGCAGGAGTCTGGGGAATGGGTGCGGGGCTCTCT 560
Qy 309 TTTTCATCTCCGCAAGTCTGCTGCTGATGAGCTGATGAGGAGTGAGCATTTCCG 368
Db 661 GTAGCAAGATCATGAGCCCTGCTTGAGTGAAGTTCGGGGTATGACAAGTAATGG 720
Qy 369 CTACCAATGTTTCATCGCTGGCTGTGTCTTTCATCATCAGACCCCTGGCCATCG 428
Db 721 AAGAAAGGGCTTTGGCTGCTGGCTGTGTCTTTCATCATCAGACCCCTGGCCATCG 780
Qy 429 CATTGATGAGGAGGCTGCTGCTGGAGTTTGACTTCTCAGCTTCGGACAGCT 488
Db 781 CATTGATGAGGAGGCTGCTGCTGGAGTTTGACTTCTCAGCTTCGGACAGCT 840
Qy 489 GCCATTGGCGCTGGTGAACCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 548
Db 841 CCCTCTGGCGCTGGTGAACCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 549 GGCCTTACGCTGTGGCCAGGAGGACCTGAGCAGGAGGAGGAGGAGGAGGAGGAGG 608
Db 901 GGCCTTACGCTGTGGCCAGGAGGACCTGAGCAGGAGGAGGAGGAGGAGGAGGAGG 960
Qy 609 TTTAGCGCGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
Db 961 GCTAGCGCGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Qy 669 GCTCCCGCGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 728
Db 1021 GCTCCCGCGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy 729 CTACTCTCTCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db 1081 ACGGACAGGAAGAACCCAGTGGTGGGCGGATCCCTTCTGCTGCTGCTGCTGCTGCT 1140
Qy 789 CCAGGCGCGCGCTTCTCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 848
Db 1141 CATCTTGGCGGCTTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Qy 849 GGAGACTTACCTAGGAGCGCCCTATGTCAGTGGAAATATGTCGCAAGAACTTTGCC 908
Db 1201 GGAGACTTACCTAGGAGCGCCCTATGTCAGTGGAAATATGTCGCAAGAACTTTGCC 1260
Qy 909 GGCCTTGGAGTGTGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 968
Db 1261 ACTTAGAAGATAGGCTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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QY 969 TGCACATGAGCCGAGAGCCCTTTCAGACCCGCTGCCCTGGTCTCTATCTGATGC 1028  
|||||  
Db 1321 TGCCAAATGAGCCGAGAGCCCTTTCAGACCCGCTGCCCTGGTCTCTATCTGATGC 1380  
|||||  
QY 1029 CAGTTGGCAGCATCTTCATGCTGCTGCTATCTCTTTTGGCTTCCCTCCTGCTGGCT 1088  
|||||  
Db 1381 CAGTTGGCAGCATCTTCATGCTGCTGCTATCTCTTTTGGCTTCCCTCCTGCTGGCTA 1440  
|||||  
QY 1089 CAACGCCCTTTCGAGAGTCTACGATTTGGACACAGGATGTTCTACCGGACTGGTGGA 1148  
|||||  
Db 1441 AAACGCCCTTTCGAGAGTCTACGATTTGGACACAGGATGTTCTACCGGCTGGG----- 1495  
|||||  
QY 1149 CTCAACGCTCTCTCTCACTACTACCGCACTTGGACAGTGGTGGTCCATGACTGCTGTA 1208  
|||||  
Db 1496 -----CCTGGACCTAGGCCAGTTGGAGCTGGAGATAG----- 1528  
|||||  
QY 1209 CAGCTACGTGTATACGATGGGCTGGGCTCCTTGGTGGCCGGCCGAGGGGTAGCCAT 1268  
|||||  
Db 1529 ----- 1528  
QY 1269 GCTGGGTGTCTTCTGCTCCGAGTGGCCCATGAGTATATCTTCTGCTTCTGCTGGG 1328  
|||||  
Db 1529 -----GGAGGGTTAGGCTCCGAGTGGCCCATGAGTATATCTTCTGCTTCTGCTGGG 1581  
|||||  
QY 1329 GTTCTTCTATCCGCTGCTGATCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1388  
|||||  
Db 1582 GTTCTTCTATCCGCTGCTGATCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1641  
|||||  
QY 1389 GATGATGACACAGCCGCGCCGATGGAACGCTGCTGATGATGAGCATCTGTTCT 1448  
|||||  
Db 1642 GCCACTGGAAGGAGCCATCCAGAGAGGGCTGGTGGTCTGATGATGAGCATCTGTTCT 1701  
|||||  
QY 1449 AGGCCAGGAATCCAGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1508  
|||||  
Db 1702 AGGCCAGGAATCCAGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1761  
|||||

## RESULT 11

US-60-360-207-10898  
; Sequence 10898, Application US/60360207  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/60/360,207  
; CURRENT FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 10898  
; LENGTH: 2924  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-360-207-10898

Query Match 26.9%; Score 421.4; DB 80; Length 2924;  
Best Local Similarity 59.2%; Pred. No. 2.3e-83;  
Matches 769; Conservative 0; Mismatches 506; Indels 24; Gaps 2;

QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTGATGAGCTGATGG 346  
|||||  
Db 348 CACCTCCAGAACAGGAGATTTTATTTCAAGCAGTCTCTTTTAGACGAGCTGTTG 407  
|||||  
QY 347 AGGTGAGCATTTCCGACCATCTACCATGTTTCATCGCTGCTGCTGCTGCTGCTGCTGCTG 406  
|||||  
Db 408 AAGTGACCATCATGAAACAAATTTACCATGTTTCATCGCACTCTCTCATCTCTATTCGCTC 467  
|||||  
QY 407 TCAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 466  
|||||  
Db 468 TCAGCACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 527  
|||||

QY 467 TGATCTTCAGCTTCGACAGCTGCCATTTGGCGTGGTGGCTGGTGGCTGGCTGGCTGGCTGG 526  
|||||  
Db 528 TGGCTATCTCTTTTGGCAATTTTCTTACTGTTATTTGGACATGGTGGGCAATGTTCTCTGT 587  
|||||  
QY 527 CCACCTCTGTTGGCGCGTACCAGGCGCTTACGCTGTTGGGCGCAGGGG----- 572  
|||||  
Db 588 CTACACTGTCAATCCCTATTTCTCTGTTCCAGCATGGGCGCCACGCTTACAGCAAGATT 647  
|||||  
QY 573 ----CACCTGGACGACGCGGCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 628  
|||||  
Db 648 CTTACCAATGATGATTTCCCTTGTCCATGGCTTGTCTTCTTAGTCTTTCAACTTTGGAG 707  
|||||  
QY 629 TGCTCTGCGCGCTCCGCGTCCACGCTGGCGTGGAGCATCAGCTCCCGCGCGGCTCCCGTT 688  
|||||  
Db 708 TTCTAGTTTGTGCCAACATACGTTGTCTTAGCATACACACTGCCACAGCTTCCCGGT 767  
|||||  
QY 689 GTGCTCTGCTTTCGAGCAGGTTAGGTTCTCTGATGAAAGCTACTCTTCTCTGAGAGAGG 748  
|||||  
Db 768 TCATTCTGATCTGGAACAGATTGCTTGTGATAATGAAGCTCACTCATTTGTCAGAGAGA 827  
|||||  
QY 749 CTGTGCTGGGATCTCTGCTGCCAGACGAGTGCAGGGATCCAGGCC-----CCAGTT 802  
|||||  
Db 828 ATATCCACGAGTACTTAAATGCAGCAAGGAGAAATCAAGCAAGATCCACTACCCACAG 887  
|||||  
QY 803 TCTCCAGCTACCTCTACTTCTCTCTGCGCCCAACACTCATCTACAGGGAGACTTACCCTA 862  
|||||  
Db 888 TCAACAGTACCTCTACTTCTCTGTTGGCGCTACACTTATTTACCGACACTACCCAA 947  
|||||  
QY 863 GGACGCCCTATCTCAGGTGGAATATGTGGCCAAAGAACTTTGCCAGGCCCTGGGATGTG 922  
|||||  
Db 948 GGACTCTCTACTTAAGATGGGTTATGTGCTATGCAAGTTTACAGGTTTGGGTGCC 1007  
|||||  
QY 923 TGTCTATGCTGCTCTACTCTGCGCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 982  
|||||  
Db 1008 TGTCTATGCTGCTCTACTCTTGTGAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1067  
|||||  
QY 983 GAGAGCCCTTCAGCACCCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1042  
|||||  
Db 1068 AGGAGCCCTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1127  
|||||  
QY 1043 TCTTCTATGCTGCTGCT 1102  
|||||  
Db 1128 TCTTCTATGCTGCTGCT 1187  
|||||  
QY 1103 AGATGCTACGATTGGAGACAGATCTTCTACCGGACTGGTGGAACTCAACGCTCTCTCT 1162  
|||||  
Db 1188 AGATGTTACGCTTGTGACAGAGTGTATTAAGGACTGGTGGAACTCTACATCACT 1247  
|||||  
QY 1163 CCAACTACTACCGCACTTGGAACTGGTGGTCCATGACTGGCTGTACAGCTAGCTGATC 1222  
|||||  
Db 1248 CCAACTACTACAGGACCTGGAACGTTGGTGCACGCTGGCTCTACTACTATGTTTACA 1307  
|||||  
QY 1223 AGATGGGCTGGGCTCTCTGCTGCGCGCGCGGAGGGTAGCCATGCTGGGTGCTTCC 1282  
|||||  
Db 1308 AAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1367  
|||||  
QY 1283 TGGTCTCCGAGTGGCCCATGATATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1342  
|||||  
Db 1368 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1427  
|||||  
QY 1343 TCATGCTGATCT 1402  
|||||  
Db 1428 TGTCTCTGCT 1487  
|||||  
QY 1403 GCACCGCGCGGAGTGAACGCTGCTGATGTGGACCATGCTGTTCTTAGGCCAGGGAATCC 1462  
|||||  
Db 1488 GGAAGGCGCAATCTGGAACATCATGGTTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1547  
|||||  
QY 1463 AGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1522  
|||||  
Db 1548 TTCTGCTGCTTCTTCTCTCAAGAGTGTGTGCTGCGCGCAGCAGCTGCTCTCTGAGAAACCTCA 1607  
|||||







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Query Match          26.0%; Score 407.2; DB 41; Length 4011;
Best Local Similarity 59.0%; Pred. No. 3.6e-80;
Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;

QY 287 CATCCCTCGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGATGAGCTGATGG 346
DB 1737 CACCTCCAGAACAGAAAGATTTTATTCGAAGCGCTCTCTCTAGATGAATGCTTG 1796

QY 347 AGGTCCAGCATTTCCGACCATCTACCATGTTTCATCGCTGGCTGTGCTCTTCATCA 406
DB 1797 AAGTGGACACATCAGAACATATACATGTTTATTCGCTCTCTCTCTCTCTCTCTATCC 1856

QY 407 TCAGCACCTCGGCCATCGACTTCATGATGAGGCGAGGCTGCTGCTGGAGTTTGACCTAC 466
DB 1857 TCAGCACACTTGTACTAGATATACATTTGATGAAGAGGCTGCTGCTGAGTTCAGCTCC 1916

QY 467 TGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGCTGACCTGGGTGGCCATGTTTCGT 526
DB 1917 TGCTTATGCTTTTGGCAAAATTCCTACCGTTTGTGGACCTGGTGGATCATGTTCCCTGT 1976

QY 527 CCACCTGTGTGGCGCTACAGGCCCTACGGCTGTGGGCCAGGGSCACCTGGAGCAGG 586
DB 1977 CTACATTTTCAGTCCCTATTTTCCTCTCTCCATGGCTTTTCATGATCTCCAGATGGAG 2036

QY 587 CGACGGGCTGTGGCTGTGCGCTTTTAGCGCCGCCAGCGCTGCTGCTCGCGCTGCCGG 646
DB 2037 CTCATCCGCTGATCGTCTCTCTCTCCATGGCTTTTCATGATCTCCAGATGGAG 2096

QY 647 TCC-----ACGTGGCGTGGAGCATCAGCTCCCGCGGCTCCCGT 688
DB 2097 TTCTAGTGTGGACCAACATATGTTGTGTAGCATATACATGCGCAGCTCCCGT 2156

QY 689 GTGCTCTGTCTTCAGCAGGTTAGTTCCTCATGAAAGTACTCCTCTCCAGAGAGG 748
DB 2157 TCATCATTTATTCAGCAGATTCGTTTGTATGAAGGCCACCTCATTTGTCAGAGAGA 2216

QY 749 CTGTCCTGGGATCCTCGTGCACGACGAGTGGAGGATCCAGGCCCGCCAGTTCTTCCA 808
DB 2217 AGTGCCTCGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACGTTTCCAAATACCTACA 2275

QY 809 G-----CTACCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 861
DB 2276 GTCAACACGATTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2335

QY 862 AGGAGCCCTATGTCAGGTGGAATTTATGTCGCAAGAACTTTGCGCAGGCCCTGGGATGT 921
DB 2336 AGGAATCCCACTGTAAAGTGGGTTATGTCGCTATGAAGTTTGCACAGCTCTTTGTTGC 2395

QY 922 GTGCTCTATGCTGCTTCATCTCGGCGGCTCTCTGTTTCTGCTCTTTGCGCAACATGAGC 981
DB 2396 TTTTCTATGTACTACATCTTTGAAAGGCTTTGCGCCCTCTGTTTTCGGAATATCAAA 2455

QY 982 CGAGAGCCCTTCAGCACCGTCCCTGCTGCTCTCTATCTCTGATCCGACGCTGGCAGGC 1041
DB 2456 CAGGAGCCCTTCAGGCTGCTGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2515

QY 1042 ATCTTCATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1101
DB 2516 GTGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2575

QY 1102 GAGATGCTACGATTTGGAGACGATGTTCTACCGGGGATGTTGGAATCAACGCTCTTC 1161
DB 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTTGGGAATCTCCACGTCATAC 2635

QY 1162 TCCAACTACTACCGCATTTGGAACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
DB 2636 TCCAACTATTATAGAACCTGGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2695

QY 1222 CAGGATGGGCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1281
DB 2696 AAGGACTTCTCTGTTTCTCTCAAGAGATTCAAATCTGCTGCTGCTGCTGCTGCTGCT 2755
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QY 1282 CTGGTCTCGCAGTGGCCCATGAGTATATCTTCTGCTCTCGGGTCTTCTTATCC 1341
DB 2756 GCTGTATCTGCTGTAGTACAGCAATAGCTTGGCTGTGCTTGGCTTCTTATCC 2815

QY 1342 GTCATGCTGATACTCTCTCTGCTCATTTGGAGGAATGTTGAACCTTCATGATGATGAC 1401
DB 2816 GTGCTCTGCTCTCTCTCTGCTCATTTGGAATGGCTTTCAACTTCATGCTCATGATAGT 2875

QY 1402 CGACCGCGCGCGCATGGAACGCTGCTGATGTGACCATCTGTTCTAGCCAGGAATC 1461
DB 2876 CGAAAAACCCCATTTGGAATGTTCTGATGTGGACTTCTTCTTGGGCAATGGAGTC 2935

QY 1462 CAGGTGAGCTGTACTGCGCAGGAGTGTAGCACGCGGCGCACTGCCCCCTTACCCCAAGCA 1521
DB 2936 TTACTCTGCTTTTATTTCAAGAAATGGTATGACGCTGCGCACTGTCTCTGAAATATCC 2995

QY 1522 ACTTTCTGGGCGCTGGTACACCTCGATCTTGGTCTGCTCAT 1563
DB 2996 ACATTTTGGATTATGTCGGCGCACGTTCTCTGGACTTGTCTGT 3037
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## RESULT 14

US-09-770-173-2800

; Sequence 2800, Application US/09770173

; GENERAL INFORMATION:

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 1600.2059-001

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,876

; PRIOR FILING DATE: 2000-01-28

; NUMBER OF SEQ ID NOS: 3167

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2800

; LENGTH: 2022

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-770-173-2800

Query Match

Best Local Similarity 25.9%; Score 405.6; DB 30; Length 2022;

Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

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QY 287 CATCTCTCGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGTGATGAGCTCATGG 346
DB 504 CACCTCCAGAACAGAAAGATTTTATTTGCAAGGCGCTCTCTCTTAGATGAACCTGTTG 563

QY 347 AGGTGACGATTTCCGCGACCATCTACCATGTTTCATCGCTGGCCTGTGTCTTTCATCA 406
DB 564 AAGTGGACCATCATCAGAACATATATCATATGTTTATTTGCCCTCTCTCTCTTATCC 623

QY 407 TCAGCACCTGCGCATCGACTTCATTTGATGAGGCGAGGCTGCTGCTGGAGATTTGACCTAC 466
DB 624 TCAGCACACTTGTAGTAGATTACATTTGATGAAGAGGCTGGTGTGTTGATTCAGCTCC 683

QY 467 TCATCTTTCAGCTTCGACAGCTGCCATTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
DB 684 TGTCTATGCTTTTGGCAAAATTTCTTACCGTTGTTGGACCTGGTGGATCATGTTCTCTGT 743

QY 527 CCACCTGTGTGGCGCGTACCAGGCCCTACGGCTGTGGGCCAGGGCAGCTGGACACGAG 586
DB 744 CTACATTTTTCAGTCCCTATTTCTGTTTCAACATTTGGGCCACTGGCTATAGCAAGATT 803

QY 587 CGACGGGCTGGGCTGTGCGCTTTTAGCGCCACGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
DB 804 CTCATCCGCTGATCGTCTCTCTCTCCATGGCTTTCTTTTCATGATCTCTCCAGATTGGAG 863

QY 647 TCC-----ACGTGGCGCTGGAGCATCAGCTCCCGCGGCTCCCGT 688
DB 864 TTCTAGGTTTGGACCAACATATGTTGTTAGCATATACATGCGCACCATGCTTCCCGT 923
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[illegible]

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: CURRENT APPLICATION NUMBER: PCT/US02/21664
: CURRENT FILING DATE: 2002-07-10
: PRIOR APPLICATION NUMBER: US 60/303,820
: PRIOR FILING DATE: 2001-07-10
: NUMBER OF SEQ ID NOS: 132
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 109
: LENGTH: 2729
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: ACAT-1: Acc. No. XM_031119
PCT-US02-21664-109

Query Match          25.9%; Score 405.6; DB 1; Length 2729;
Best Local Similarity 58.9%; Pred. No. 7.6e-80;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps

Qy 287 CATCCCTGGGGAACAGAAAGCTTTTCATCATCGCAGCTCCCTGCTTCATGAGTCGATGG 346
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 484 CACCTCCAGAACAGGAAGAATTTTATGCAAGCGCTCTCTCTAGATGACACTGCTTG 543
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 347 AGGTGCAGCATTTCCGCACCATCTACCACTATGTTCAATCGCTGGCCTGTGTGTTTCATCA 406
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 544 AAGTGGACCACATCAGAACATATATACATGTTTATTGGCCCTCCTCATCTCTCTTATCC 603
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 407 TCAGACACCTGGCCATCGACTTCATGATGAGGCAGCGTCTGCTGGATTTGACCTAC 466
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 604 TCAGCACACTTGTAGTAGATTACATGATGAAGGAAGCGTGTGCTTGAGTTCAGCTCC 563
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 467 TCATCTTCAGCTTCGGAGAGCTGCCATTGGCGCTGGTACCTTGGTGGTCCCAATGTTTCGT 526
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 664 TGTCTATGCTTTTGGCAAAATTCCTACCGTTGTTGGACCTGGTGGATCATGTTCTCTGT 723
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 527 CCACCCCTGTGGCGCGGTACAGGCCCTACGGCTGTGGCCAGGGCCACCTGGAGCAGG 586
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 724 CTACATTTTTCAGTTCCCTATTTCTGTTTCAACATTTGGGCCACTGCTATACAGAGATT 783
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 587 CGACGGCGCTGGCTGTGGCTTTTAGCGCCCGCAGCGCTGGTGTCTGCGCGCTGCCGG 646
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 784 CVCATCCGCTGATCCGTTCTCTCTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG 843
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 647 TCC-----ACGTGGCGCTGGAGCATCAGCTCCGCGCGGCTCCCGTT 688
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 844 TTCTAGGTTTGGACCAACATATGTTGTTTASCATATACATGCCACCACTGTTCCCGGT 903
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 689 GTGTCTGTCTTCGAGCAGGTTAGTGTCTGATGAAAAGCTACTCCTTCTCTCAGAGAGG 748
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 904 TCATCATTTATATTCGAGCAGATTTCGTTTTGTAATGAAGGCCCACTCATTTGTTCAGAGA 963
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 749 CTGTGCTCGGATCCCTTCGTGCCAGCAGAGGTGAGGGGATCCAGGCCCGCCAGTTTCTCCA 808
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 964 ACGTGCCTCGGTACTAAAT-TCAGTAAAGGAAATCAAGCACTGTTCCAATACCTACA 1022
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 809 G-----CTACCTCTACTTCTCTTCGCCCACAACTCATCTACAGGGAGACTTACCCT 861
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1023 GTCAAGCAGTATTTGACTCTTATTTGTTCTTACCCCTATCTACCGTGCACACTATCCC 1082
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 862 AGACGCCCTATCTCAGGTGGAAATATGTGCCCAAGAACTTTGCCAGGCGCCTGGGATGT 921
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1083 AGGAATCCCCTGTAAGATGGGTTATGCGCTATGAAGTTTCACAGAGTCTTTGGTTGC 1142
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 922 GTGCTCTATGCCCTGCTTCATCCTGGGCCGCTCTGTGTTCCCTGTCTTTGCCACATGAGC 981
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1143 TTTTCTCTATGTACTACATCTTTGAAAGGCTTTGTGCCCGCTTGTTCGGAATATCAAA 1202
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 982 CGAGAGCCCTTCAGCACCCGTCCTGCTCTCTATCTCTGATGCCAGCTTGGCCAGGC 1041
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1203 CAGGAGCCCTTCAGCGCTCGTGTCTCGTCTCTATGTTATTTACTCCATCTTGCCAGGT 1262
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1042 ATCTTTCATGCTGCTGCCTCATCTTTTGGCCTTCCTCCATTTGCTGGCTCAAGCCCTTTGCC 1101
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2003, 13:20:11 ; Search time 521 Seconds  
(without alignments)

13964.161 Million cell updates/sec

Title: us-09-918-026a-3

Perfect score: 1569

Sequence: 1 atggagccaggcgggcgccg.....cttggtcgtgcatactag 1569

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6062914 seqs, 2318460206 residues

Total number of hits satisfying chosen parameters: 12125828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq2.\*
- 7: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq3.\*
- 8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq2.\*
- 10: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description          |
|------------|--------|-------------|--------|----|----------------------|
| 1          | 1566.2 | 99.8        | 1983   | 11 | US-60-452-680-12201  |
| 2          | 1566.2 | 99.8        | 1983   | 11 | US-60-453-135-7616   |
| 3          | 1566.2 | 99.8        | 1983   | 11 | US-60-453-050-7616   |
| 4          | 1564.2 | 99.7        | 1569   | 7  | US-09-949-016-5159   |
| 5          | 1564.2 | 99.7        | 1983   | 8  | US-10-170-235-23912  |
| 6          | 1113.4 | 71.0        | 1607   | 9  | US-10-144-771-5649   |
| 7          | 421.4  | 26.9        | 2924   | 9  | US-10-144-771-10898  |
| 8          | 407.2  | 26.0        | 4011   | 9  | US-10-342-887-388    |
| 9          | 407.2  | 26.0        | 4011   | 11 | US-60-440-068-313    |
| 10         | 405.6  | 25.9        | 2738   | 8  | US-10-170-235-25116  |
| 11         | 405.6  | 25.9        | 2738   | 10 | US-60-455-444-2252   |
| 12         | 405.6  | 25.9        | 2738   | 11 | US-60-452-680-8056   |
| 13         | 405.6  | 25.9        | 2738   | 11 | US-60-453-135-4736   |
| 14         | 405.6  | 25.9        | 2738   | 11 | US-60-453-050-4736   |
| 15         | 345.2  | 22.0        | 508    | 6  | US-09-532-315B-1168  |
| 16         | 268.2  | 17.1        | 24553  | 7  | US-09-949-016-16901  |
| 17         | 253.4  | 16.2        | 531    | 8  | US-10-375-682-406    |
| 18         | 200.6  | 12.8        | 201    | 11 | US-60-452-680-115000 |
| 19         | 200.6  | 12.8        | 201    | 11 | US-60-452-680-115001 |
| 20         | 200.6  | 12.8        | 201    | 11 | US-60-452-680-115003 |
| 21         | 200.6  | 12.8        | 201    | 11 | US-60-452-680-115004 |
| 22         | 200.6  | 12.8        | 201    | 11 | US-60-452-680-115005 |

|    |       |      |     |    |                      |                    |
|----|-------|------|-----|----|----------------------|--------------------|
| 23 | 200.6 | 12.8 | 201 | 11 | US-60-453-135-82165  | Sequence 82165, A  |
| 24 | 200.6 | 12.8 | 201 | 11 | US-60-453-135-82166  | Sequence 82166, A  |
| 25 | 200.6 | 12.8 | 201 | 11 | US-60-453-135-82168  | Sequence 82168, A  |
| 26 | 200.6 | 12.8 | 201 | 11 | US-60-453-135-82169  | Sequence 82169, A  |
| 27 | 200.6 | 12.8 | 201 | 11 | US-60-453-135-82170  | Sequence 82170, A  |
| 28 | 200.6 | 12.8 | 201 | 11 | US-60-453-050-82165  | Sequence 82165, A  |
| 29 | 200.6 | 12.8 | 201 | 11 | US-60-453-050-82166  | Sequence 82166, A  |
| 30 | 200.6 | 12.8 | 201 | 11 | US-60-453-050-82168  | Sequence 82168, A  |
| 31 | 200.6 | 12.8 | 201 | 11 | US-60-453-050-82169  | Sequence 82169, A  |
| 32 | 200.6 | 12.8 | 201 | 11 | US-60-453-050-82170  | Sequence 82170, A  |
| 33 | 199   | 12.7 | 201 | 11 | US-60-452-680-114999 | Sequence 114999, A |
| 34 | 199   | 12.7 | 201 | 11 | US-60-452-680-115002 | Sequence 115002, A |
| 35 | 199   | 12.7 | 201 | 11 | US-60-453-135-82164  | Sequence 82164, A  |
| 36 | 199   | 12.7 | 201 | 11 | US-60-453-135-82167  | Sequence 82167, A  |
| 37 | 199   | 12.7 | 201 | 11 | US-60-453-050-82164  | Sequence 82164, A  |
| 38 | 199   | 12.7 | 201 | 11 | US-60-453-050-82167  | Sequence 82167, A  |
| 39 | 197.4 | 12.6 | 442 | 6  | US-09-532-315B-10003 | Sequence 10003, A  |
| 40 | 177.4 | 11.3 | 266 | 6  | US-09-532-315B-6819  | Sequence 6819, Ap  |
| 41 | 159.8 | 10.2 | 257 | 6  | US-09-532-315B-15147 | Sequence 15147, A  |
| 42 | 159.4 | 10.2 | 302 | 6  | US-09-532-315B-13629 | Sequence 13629, A  |
| 43 | 140.6 | 9.0  | 141 | 11 | US-60-452-680-115006 | Sequence 115006, A |
| 44 | 140.6 | 9.0  | 141 | 11 | US-60-453-135-82171  | Sequence 82171, A  |
| 45 | 140.6 | 9.0  | 141 | 11 | US-60-453-050-82171  | Sequence 82171, A  |

#### ALIGNMENTS

##### RESULT 1

US-60-452-680-12201  
; Sequence 12201, Application US/60452680  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: GRUPE, Andrew  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01450  
; CURRENT APPLICATION NUMBER: US/60/452,680  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 116213  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12201  
; LENGTH: 1983  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-452-680-12201

Query Match 99.8%; Score 1566.2; DB 11; Length 1983;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1562; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | ATGGAGCCAGCGGGCCCGCTCTGCTGTCAGAGCAGACAGAGGCTGGAGGGAGCGG     | 60  |
| DB | 1   | ATGGAGCCAGCGGGCCCGCTCTGCTGTCAGAGCAGACAGAGGCTGGAGGGAGCGG     | 60  |
| QY | 61  | GAGCGCCAAACCTCTGGAGATGAAACACTGAGACGACAGAGCCCGGACTTGGTACAA   | 120 |
| DB | 61  | GAGCGCCAAACCTCTGGAGATGAAACACTGAGACGACAGAGCCCGGACTTGGTACAA   | 120 |
| QY | 121 | TGAGCCGACACATGAGGCTGTGAAGGCACAAATCTCTGGAGCAAGCGGACCAACTG    | 180 |
| DB | 121 | TGAGCCGACACATGAGGCTGTGAAGGCACAAATCTCTGGAGCAAGCGGACCAACTG    | 180 |
| QY | 181 | AGGAGCTCTGATCGCGCCATGCGGAGGCTATACAACTCCCTACCATCACAAGACAA    | 240 |
| DB | 181 | AGGAGCTCTGATCGCGCCATGCGGAGGCTATACAACTCCCTACCATCACAAGACAA    | 240 |
| QY | 241 | CCTCTGCCCCACCTCCCTCCAGSTTCTTTGACAGGACCCAGGAGCCATCCCTCGGGAAA | 300 |
| DB | 241 | CCTCTGCCCCACCTCCCTCCAGSTTCTTTGACAGGACCCAGGAGCCATCCCTCGGGAAA | 300 |
| QY | 301 | CAGAAAGTTTTCATCCGCAAGTCCCTCTGTTGATGAGTGTGAGGTGACAGATTTC     | 360 |
| DB | 301 | CAGAAAGTTTTCATCCGCAAGTCCCTCTGTTGATGAGTGTGAGGTGACAGATTTC     | 360 |

Db 301 CAGAAAGTTTTCATCCCAAGTCCCTGCTTGATGAGCTGATGAGGTGCAGCATTTTC 360  
Qy 361 CGCACCATTACACATGTTATCATCGTGGCCCTGTGTCTTCAATATAGCACCCTGGCC 420  
Db 361 CGCACCATTACACATGTTATCATCGTGGCCCTGTGTCTTCAATATAGCACCCTGGCC 420  
Qy 421 ATCGACTTCATTGATGAGGCGAGCTGCTGCTGAGTTTGACCTACTGATCTTCAGCTTC 480  
Db 421 ATCGACTTCATTGATGAGGCGAGCTGCTGCTGAGTTTGACCTACTGATCTTCAGCTTC 480  
Qy 481 GGACAGCTGCATTTGGCGCTGGTACCTGGTGGCCCACTGTTCTGCCACCCCTGTGGGG 540  
Db 481 GGACAGCTGCATTTGGCGCTGGTACCTGGTGGCCCACTGTTCTGCCACCCCTGTGGGG 540  
Qy 541 CCGTACCAGGCCCTACGGCTGTGGGCCAGGGCAGCTGGAGCGAGGGCGGCTGGGC 600  
Db 541 CCGTACCAGGCCCTACGGCTGTGGGCCAGGGCAGCTGGAGCGAGGGCGGCTGGGC 600  
Qy 601 TGTGCGCTTTAGCGGCCACCGCTGCTGCTGCGCTGCGGCTGCCAGCTGGCCGTG 660  
Db 601 TGTGCGCTKTAGCGGCCACCGCTGCTGCTGCGCTGCGGCTGCCAGCTGGCCGTG 660  
Qy 661 GAGCATCAGCTCCCGCGGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 661 GAGCATCAGCTCCCGCGGCTCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Qy 721 ATGAAGAGCTACTCTTCCTGAGAGAGCTGCTGCTGGGATCTTCTGCTGCTGCTGCTGCT 780  
Db 721 ATGAAGAGCTACTCTTCCTGAGAGAGCTGCTGCTGGGATCTTCTGCTGCTGCTGCTGCT 780  
Qy 781 GAGGGATCCAGGCCCCAGTTTCTCCAGCTACCTTCTACTTCTTCTTCTTCTTCTTCTTCT 840  
Db 781 GAGGGATCCAGGCCCCAGTTTCTCCAGCTACCTTCTACTTCTTCTTCTTCTTCTTCTTCT 840  
Qy 841 ATCTACAGGAGACTTACCTTAGACGCCCTATGTCAGGTGGAATATGTGGCCAAAGAC 900  
Db 841 ATCTACAGGAGACTTACCTTAGACGCCCTATGTCAGGTGGAATATGTGGCCAAAGAC 900  
Qy 901 TTTGGCCAGGCTGGGATGTGCTCTATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960  
Db 901 TTTGGCCAGGCTGGGATGTGCTCTATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960  
Qy 961 CCGTGTCTTGGCAACATGAGCGGAGAGCCCTTACGACCCGCTGCTGCTGCTGCTGCTGCT 1020  
Db 961 CCGTGTCTTGGCAACATGAGCGGAGAGCCCTTACGACCCGCTGCTGCTGCTGCTGCTGCT 1020  
Qy 1021 CTGTCATGCCAGCTTCCAGGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Db 1021 CTGTCATGCCAGCTTCCAGGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Qy 1081 TGCTGGCTCAACGCCCTTTGCCAGATGCTAGATTTGGAGAGAGATTTCTACGGGAC 1140  
Db 1081 TGCTGGCTCAACGCCCTTTGCCAGATGCTAGATTTGGAGAGAGATTTCTACGGGAC 1140  
Qy 1141 TGGTGAACCTAACGCTCTTCTCAACTACTACCCACTTGAACGCTGCTGCTGCTGCTGCTGCT 1200  
Db 1141 TGGTGAACCTAACGCTCTTCTCAACTACTACCCACTTGAACGCTGCTGCTGCTGCTGCTGCT 1200  
Qy 1201 TGCTGTACAGCTACGCTGATCAGATGGCTGCGGCTCTTGGTGGCCGCGGCGAGGG 1260  
Db 1201 TGCTGTACAGCTACGCTGATCAGATGGCTGCGGCTCTTGGTGGCCGCGGCGAGGG 1260  
Qy 1261 GTAGCCATGCTGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
Db 1261 GTAGCCATGCTGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
Qy 1321 GTCCCTGGGTGCTTCTTATCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
Db 1321 GTCCCTGGGTGCTTCTTATCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
Qy 1381 AACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
Db 1381 AACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

Qy 1441 CTGTTTCTAGCCAGGGAATCCAGGTCAAGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
Db 1441 CTGTTTCTAGCCAGGGAATCCAGGTCAAGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
Qy 1501 CACTGCCCTTACCAGGCAACTTTCTGGGGCTGTGTGACACCTCGATCTTGTTCCTGCT 1560  
Db 1501 CACTGCCCTTACCAGGCAACTTTCTGGGGCTGTGTGACACCTCGATCTTGTTCCTGCT 1560  
Qy 1561 CATACCTAG 1569  
Db 1561 CATACCTAG 1569

RESULT 2  
US-60-453-135-7616  
; Sequence 7616, Application US/60453135  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001456  
; CURRENT APPLICATION NUMBER: US/60/453,135  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7616  
; LENGTH: 1983  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-135-7616

Query Match 99.8%; Score 1566.2; DB 11; Length 1983;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1562; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGCCAGCGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
Db 1 ATGGAGCCAGCGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
Qy 61 GAGCGCCAAACCTGTGTGAGATGGAACACTGTGACGCGCACAGAGCCCGGACTTGGTACAA 120  
Db 61 GAGCGCCAAACCTGTGTGAGATGGAACACTGTGACGCGCACAGAGCCCGGACTTGGTACAA 120  
Qy 121 TGGACCCGACACATGAGGCTGTGAAGGCACAAATGCTGAGCAAGCGCAGGAGCAACTG 180  
Db 121 TGGACCCGACACATGAGGCTGTGAAGGCACAAATGCTGAGCAAGCGCAGGAGCAACTG 180  
Qy 181 AGGAGCTGTGATCGGGCATCGGGAGGCTATACAATCCTACCCATCACAAGACAAA 240  
Db 181 AGGAGCTGTGATCGGGCATCGGGAGGCTATACAATCCTACCCATCACAAGACAAA 240  
Qy 241 CCTCTGCCCCACCTCCCCAGGTTCTTGGAGGAGCCAGGAGCCATCCCTGGGGAAA 300  
Db 241 CCTCTGCCCCACCTCCCCAGGTTCTTGGAGGAGCCAGGAGCCATCCCTGGGGAAA 300  
Qy 301 CAGAAAGTTTTCATCATCCCGAAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Db 301 CAGAAAGTTTTCATCATCCCGAAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Qy 361 CGCACCATTACACATGTTTCTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 361 CGCACCATTACACATGTTTCTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Qy 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 421 ATCGACTTCATTGATGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Qy 481 GGACAGCTGCATTTGGCGCTGGTACCTGGTGGCCCACTGTTCTGCCACCCCTGTGGGG 540  
Db 481 GGACAGCTGCATTTGGCGCTGGTACCTGGTGGCCCACTGTTCTGCCACCCCTGTGGGG 540



[illegible]

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RESULT 4
US-09-949-016-5159
; Sequence 5159, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5159
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-5159

Query Match          99.7%; Score 1564.2; DB 7; Length 1569;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1566; Conservative 0; Mismatches 3; Indels 0; Gaps

QY 1 ATGAGCAGCGGGCGCGCTGCTGCTGCGAGAGACAGAGGGCTGGAGGGGAGCGG 60
DB 1 ATGAGCAGCGGGCGCGCTGCTGCTGCGAGAGACAGAGGGCTGGAGGGGAGCGG 60
QY 61 GAGCGCAACCCCTGTGGAGATGAACAACACTGAGACGCACAGACCCCGGACTTGGTACAA 120
DB 61 GAGCGCAACCCCTGTGGAGATGAACAACACTGAGACGCACAGACCCCGGACTTGGTACAA 120
QY 121 TGGACCCGACACATGAGAGGCTGTGAAGGCAAAATGCTGGAGCAAGCGGAGGACACACTG 180
DB 121 TGGACCCGACACATGAGAGGCTGTGAAGGCAAAATGCTGGAGCAAGCGGAGGACACACTG 180
QY 181 AGGAGCTGCTGGATCGGCGCATCGCGGAGGCTATACAATCTTACCCATCACAAAGACAA 240
DB 181 AGGAGCTGCTGGATCGGCGCATCGCGGAGGCTATACAATCTTACCCATCACAAAGACAA 240
QY 241 CCTCTGCCCCACACTGCCCCAGGTTCTTGAAGGCAAAATGCTGGAGCAAGCGGAGGACACACTG 300
DB 241 CCTCTGCCCCACACTGCCCCAGGTTCTTGAAGGCAAAATGCTGGAGCAAGCGGAGGACACACTG 300
QY 301 CAGAAAGTTTTCATATCCGCAAGTCCCTGCTTCATGAGCTGATGAGGTGCAGCATTTTC 360
DB 301 CAGAAAGTTTTCATATCCGCAAGTCCCTGCTTCATGAGCTGATGAGGTGCAGCATTTTC 360
QY 361 CGCACACTCTACCAACATGTTTCATCGCTGGCGTGTGTCTTTCATCATCAGCACCCCTGGCC 420
DB 361 CGCACACTCTACCAACATGTTTCATCGCTGGCGTGTGTCTTTCATCATCAGCACCCCTGGCC 420
QY 421 ATFCGACTTCATGATGAGGGCAGGCTGCTGCTGAGGTTTGACCTACTGATCTTCAGCTTC 480
DB 421 ATFCGACTTCATGATGAGGGCAGGCTGCTGCTGAGGTTTGACCTACTGATCTTCAGCTTC 480
QY 481 GGACAGCTGCCAATGGCGCTGCTGGACCTGGGTGCCCATGTTTCTGTCCACCCCTGTTGGCG 540
DB 481 GGACAGCTGCCAATGGCGCTGCTGGACCTGGGTGCCCATGTTTCTGTCCACCCCTGTTGGCG 540
QY 541 CGGTACCAAGGCCCTACGGCTGTGGGCCAGGGGCACCTGGAGCGAGGCGAGGGGCTGGGC 600
DB 541 CGGTACCAAGGCCCTACGGCTGTGGGCCAGGGGCACCTGGAGCGAGGCGAGGGGCTGGGC 600
QY 601 TGTGGCGCTTTAGCCCGCCAGCCGCTGCTCTGCGCGCTGCCGCTGCACGTGGCCCGCTG 660
DB 601 TGTGGCGCTTTAGCCCGCCAGCCGCTGCTCTGCGCGCTGCCGCTGCACGTGGCCCGCTG 660
QY 661 GAGCATCAGCTCCCGCGGCGCTCCCGTGTGTGCTCTGGTCTTCGAGCAGGTTAGTGTCCCTG 720
DB 661 GAGCATCAGCTCCCGCGGCGCTCCCGTGTGTGCTCTGGTCTTCGAGCAGGTTAGTGTCCCTG 720
QY 721 ATGAAAGCTACTTCCTTCTGAGAGGCTGTGCTCGGATCCCTTCGTGCCAGCAGAGGT 780
DB 721 ATGAAAGCTACTTCCTTCTGAGAGGCTGTGCTCGGATCCCTTCGTGCCAGCAGAGGT 780
QY 781 GAGGGATCCAGGCCGCCAGTTTCTCCAGCTACCTCTACTTCTCTTCTGCCCCAACACTC 840
DB 781 GAGGGATCCAGGCCGCCAGTTTCTCCAGCTACCTCTACTTCTCTTCTGCCCCAACACTC 840
QY 841 ATCTACAGGAGACTTTACCCCTAGGAGGCCCTATGTTCAGGTGGAATATGTGCCCAGAAC 900
DB 841 ATCTACAGGAGACTTTACCCCTAGGAGGCCCTATGTTCAGGTGGAATATGTGCCCAGAAC 900

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QY 1141 TGGTGAACCTAACAGTCCCTTCCAACTACTACCGCACTTGAAGCTGGTGTCCATGAC 1200
Db 1141 TGGTGAACCTAACAGTCCCTTCCAACTACTACCGCACTTGAAGCTGGTGTCCATGAC 1200
QY 1201 TGCGCTACAGCTACCTGTATCAGGATGGCTGCGGCTCCTTTGGTGCCCGGCGCGAGGG 1260
Db 1201 TGCGCTACAGCTACCTGTATCAGGATGGCTGCGGCTCCTTTGGTGCCCGGCGCGAGGG 1260
QY 1261 GTAGCCATGCTGGGTGTGTTCTCGCTCCGAGTGGCCCATAGATATATCTTGTCTTC 1320
Db 1261 GTAGCCATGCTGGGTGTGTTCTCGCTCCGAGTGGCCCATAGATATATCTTGTCTTC 1320
QY 1321 GTCCGTGGGTCTTCTATCCCGTCACTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1321 GTCCGTGGGTCTTCTATCCCGTCACTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
QY 1381 AACTTCATGATGATGACACGACGCGCGCGCGCATGGAACGTGCTGATGTGACCATG 1440
Db 1381 AACTTCATGATGATGACACGACGCGCGCGCATGGAACGTGCTGATGTGACCATG 1440
QY 1441 CTGTTCTAGCCAGGAATCCAGGTACGCTGTACTGCGAGAGTGTACGACGCGG 1500
Db 1441 CTGTTCTAGCCAGGAATCCAGGTACGCTGTACTGCGAGAGTGTACGACGCGG 1500
QY 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGGTGACACTCGATCTTGGTCTCTGC 1560
Db 1501 CACTGCCCTTACCCAGGCAACTTTCTGGGGCTGGTGACACTCGATCTTGGTCTCTGC 1560
QY 1561 CATACCTAG 1569
Db 1561 CATACCTAG 1569

RESULT 6
US-10-144-771-5649
; Sequence 5649, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 5649
; LENGTH: 1607
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-144-771-5649

Query Match 71.0%; Score 1113.4; DB 9; Length 1607;
Best Local Similarity 83.2%; Pred. No. 3,4e-255;
Matches 1296; Conservative 0; Mismatches 246; Indels 15; Gaps 2;

QY 28 CTGCGAGAGACAGAGGCTGGGAGGAGCGGAGCGCCCAACCTGT- --GGAGATGGA 84
Db 51 CTTCTGGAGAGAGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 110
QY -85 AACACTGAGACGACAGAGCGCGGACTTGGTACAAATGGACCGACACATGAGGCTGTG 144
Db 111 AACGAGGACACAGCGGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 170
QY 145 AAGGACAAATTCGTGAGCAAGCGGAGGAGCAACTGAGGAGGAGGAGGAGGAGGAGGAG 204
Db 171 AAGACACAGTTTCTGGAGCAAGCAGAGAGAGTGGGAGAGAGTGGGAGAGAGTGGGAG 230
QY 205 CGGGAGGCTATACATCTTACCATCACAAGACAACTCTGCCCGCCACCTCCCGCCAGGT 264
Db 231 TGGGAGGCTATGCAAGCTTACCGCCCAACAAAGACAGACCTCTTCCCTCGCTGCCCAAT 290
QY 265 TCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 324
Db 291 TCTTACAGCAAGACCAAGAGTTACACCTCTGGAAACGAAAGTTTTCATCATCCCGCAAG 350

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QY 325 TCCCTGCTTGATGAGCTGATGAGAGTGCAGCAATTCGCCACCACTTACCACATGTTTCATC 384
Db 351 TCACCTGATGATGAGTAATGAGAGTGCACATTTCCGAACCACTTACCACATGTTTCATA 410
QY 385 GCTGGCCTGTGTCTTCATCATCATCAGACACCTGCCATCAGCTTCATTCATGAGGAGG 444
Db 411 GCGGCGCTATGCGTCTGATCATCAGACACCTGGCCATCGACTTCATTCATGAGGAGGAG 470
QY 445 CTGCTGCTGGAGTTGACCTACTGATCTTCAGCTTCGACAGCTGCCATTCGCCCTGTGTG 504
Db 471 TTGATGCTGGAGTTTGGATTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 530
QY 505 ACCTGGGTGCCCATGTTTCTCTCCACCTGTGTGGCGCGGTACCAGGCGCTTACGCGTGTGG 564
Db 531 ACCTGGGTGCCCATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 590
QY 565 GCGA-----GGGCGACCTGGACGAGCGCGCGCTGGGCTGTGGCTTTT 612
Db 591 GCGAGCGCGCGCGCTGGGCGTGGGATGCTGGGCGCGCGCTGGGCTGTGGCTGTGTGCTG 650
QY 613 GCGCGCCACGCGCTGCTCTGCGCGCTGCGGCTCCAGCTGGCGGTGGAGCATCAGCTC 672
Db 651 GCTGCCACGCTGTGTGCTCTGCTGCTGCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTG 710
QY 673 CCGCGCGCGCTCCGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 732
Db 711 CCGCGCGCGCTCCGCTGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 770
QY 733 TCCTTCTCTGAGAGAGCTGTGCTGGGATCTTCTGCGCGAGAGGAGGAGGAGGAGGAGGAG 792
Db 771 TCCTTCTCTGAGAGAGCTGTGCTGGGATCTTCTGCTGAGAGGAGGAGGAGGAGGAGGAG 830
QY 793 GCGCGCGAGTTTCTCCAGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 852
Db 831 GCGCGCGAGTTTCTCCAGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 890
QY 853 ACTTACCTCTAGGAGCGCTTATGCTAGCTGGAATATGCGCGCAAGAACTTTGCCCGAGGCG 912
Db 891 ACATACCGGAGGAGACCGGAGCTAGCTGGAATATGCGCGCAAGAACTTTGCCCGAGGCTC 950
QY 913 CTGGGATGTGTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 972
Db 951 CTGGGCTGTGTCTCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1010
QY 973 AACATGAGCGGAGAGCGCTTACGACCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1032
Db 1011 AACATGAGCGGAGAGCGCTTACGACCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1070
QY 1033 TTGCGAGGCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1092
Db 1071 GCGCGAGGCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1130
QY 1093 GCCTTTGCCGAGATGTCTACGATTTGAGAGAGAGATGTTCTACCGGAGCTGGTGAATCTCA 1152
Db 1131 GCCTTTGCCGAGATGTCTGCGGTTTGGAGAGAGAGATGTTCTACCGGAGTGGTGAATCTCG 1190
QY 1153 ACCTGCTCTCTCCAACTACTACCGCACTTGAACGTGTGGTGTCTCTCTCTCTCTCTCTCTCT 1212
Db 1191 ACTTCTCTCTCCAACTACTACTACCGCACTTGAACGTGTGGTGTCTCTCTCTCTCTCTCTCT 1250
QY 1213 TACGTGTATCAGGATGGGCTGCGGCTCTCTTGGTGCGCGCGCGGAGGAGGAGGAGGAGGAG 1272
Db 1251 TATGTGTATCAAGATGGGCTGTGGCTTTAGGAGGAGGCGGCTCTCGCGGCTGGGAGGAG 1310
QY 1273 GGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
Db 1311 GGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1370
QY 1333 TTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1392
Db 1371 TTCTACCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1430

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; LENGTH: 4011  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-342-887-388

Query Match 26.0%; Score 407.2; DB 9; Length 4011;  
 Best Local Similarity 59.0%; Pred. No. 9.2e-87;  
 Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;

QY 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTGATGAGCTATGG 346  
 DB 1737 CACCTCCAGAACAGGAAAGATTTTATGCAAGGGCGCTCTCTTAGATGAACCTGTTG 1796  
 QY 347 AGGTGAGCAATTTCCGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406  
 DB 1797 AAGTGGACACATGACAGCAATATATACATGTTTATGCGCTCCCTCATTTCTTTATCC 1856  
 QY 407 TCAGACCCCTGGGCGATCGACTTCATGATGAGGCGAGTGTGCTGGAGTTTGTGACCTAC 456  
 DB 1857 TCAGACACATTTGTAGTAGATACATGATGATGAGGAGGCTGGTGTGATGAGTTTGTG 1916  
 QY 467 TGATCTTCAGCTTCGAGACAGTGCATTTGGCGTGGTGGTGGTGGTGGTGGTGGTGGT 526  
 DB 1917 TGTCTTAGCTTTTGGCAATTTCCATCCGTTTGGTGGTGGTGGTGGTGGTGGTGGTGG 1976  
 QY 527 CCACCCCTGTTGGCGCCCTACCGCCCTACGGCTGTGGGCGAGGGGCACTTGGACGAGG 586  
 DB 1977 CTACATTTTTCAGTTCCCTATTTCTGTTTCAACATTTGGGCGACTGGCTATAGCAAGAT 2036  
 QY 587 CGAGGGCGCTGGCTGTGCGCTTTTACGCGCCACGCGGTGGTGGTGGTGGTGGTGGTGG 646  
 DB 2037 CTATCCGCTGATCGGTTCTCTCTTCCATGCTTCTTTCATGATTTCCAGATTTGAG 2096  
 QY 647 TCC-----ACGTGGCGGTGGAGCATGAGTCCCGCGCGCTCCCGCTCCCGTT 688  
 DB 2097 TTCTAGGTTTTGGACCAACATATGTTGTTGTTAGCATATACATGCCACGAGTTCCCGGT 2156  
 QY 689 GTGCTCGGCTTCGAGAGGTTAGTTCCTGTGATGAAAGTACTCTCTTCTGAGAGAGG 748  
 DB 2157 TCATCATTTATTTGAGCAGATTCGTTTGTGTAAGAGGCGCCACTCATTTGTCAGAGA 2216  
 QY 749 CTGTGCTGGGATCCTTCGTGCCAGAGAGTGGAGGATCCAGGCGCCCGAGTTTCCTCA 808  
 DB 2217 AGTGCTTCGGGTACTAAAT--TCAGCTAAGAGAGAAATCAAGCACTGTTCNAATACCT 2275  
 QY 809 G-----CTACCTCTACTCTCTCTTCGCCAACACTCATCTACAGGAGACTTACCT 861  
 DB 2276 GTCAACCAAGTATTTGACTTCTTATTTGCTCTACCTTATCTACCGGTGACAGCTATCC 2335  
 QY 862 AGGAGCCCTATGTCAGGTGAATATGTGGCCAGAACTTTGCCAGGCGCTGGGATGT 921  
 DB 2336 AGGAATCCCACTGTAAAGATGGGTTATGTCGTATGAAGTTTGGACAGGCTTTTGGTTGC 2395  
 QY 922 GTGCTCTATGCTGCTCATCTGCGGCGCTCTGTGTCTCTGCTTTCCTCAACATGAGC 981  
 DB 2396 TTTTCTATGTGACTACATCTTTGAAGGCTTTGTGCGCCCTTTGTCGAATATCAAA 2455  
 QY 982 CGAGAGCCCTTCAGACCCGCTGCTGTGCTCTCTATCTGCTGATGCGACGCTTGCAGGC 1041  
 DB 2456 CAGGAGCCCTTCAGGCGCTGCTGTGCTCTATGCTATGAAGTTTGGTGAAGTCCACGTC 2515  
 QY 1042 ATCTTCATGCTGCTCATCTCTCTTTCCTTCCATTTGCTGCTCAAGCGCTTTTGGC 1101  
 DB 2516 GTGCTGATCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2575  
 QY 1102 GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGAGTGGTGGAACTCAACGCTTC 1161  
 DB 2576 GAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTTGGTGAAGTCCACGTC 2635  
 QY 1162 TCCAACTACTACCGACTTGGAACTGGTGGTCCATGACTGCTCTACAGTACGTTGAT 1221  
 DB 2636 TCCAACTATTATAGAACCTGGAATGTTGGTGGTCCATGATGACTGGCTATTTACTATGCT 2695

QY 1222 CAGGATGGGCTCGCGCTCCTTGGTGCCTGGGCGCCGAGGGGTAGCCATGCTGGGTGTTC 1281  
 DB 2696 AAGGACTTTTCTGCTGTTTTTCTCCAGAGATTCAAATCTGCTGCCATGTAGCTGTCTTT 2755  
 QY 1282 CTGGTCTCGGAGTGGCCCATGAGTATATCTCTGCTGCTCGGTCTTCTATCC 1341  
 DB 2756 GGTGATCTGCTGTAGTACAGCAATATGCTTGGCTGTGCTTGGCTTGTAGCTTTTCTATCC 2815  
 QY 1342 GTCATGCTGATACCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1401  
 DB 2816 GTGCTCTCTGCTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2875  
 QY 1402 CGACCGGCGCGCATGAGCACTGCTGTGATGTGACCACTGCTTCTTCTAGGCGAGGATC 1461  
 DB 2876 CGGAAAGCCGATTTGGAATGTTGATGTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 2935  
 QY 1462 CAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1521  
 DB 2936 TTAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2995  
 QY 1522 ACTTCTGCGGCTGGTGTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1563  
 DB 2996 ACATTTTGGATTATGCTCGGCGACGTTCTCTGAGCTTGTCTG 3037

RESULT 9

US-60-440-068-313  
 ; Sequence 313, Application US/60440068  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARMAN, STEVEN G.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE  
 ; TITLE OF INVENTION: NP-KB PATHWAY  
 ; FILE REFERENCE: 3053-4191  
 ; CURRENT APPLICATION NUMBER: US/60/440,068  
 ; CURRENT FILING DATE: 2003-01-14  
 ; NUMBER OF SEQ ID NOS: 746  
 ; SOFTWARE: Patent Ver. 2.1  
 ; SEQ ID NO 313  
 ; LENGTH: 4011  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-60-440-068-313

Query Match 26.0%; Score 407.2; DB 11; Length 4011;  
 Best Local Similarity 59.0%; Pred. No. 9.2e-87;  
 Matches 768; Conservative 0; Mismatches 508; Indels 26; Gaps 3;

QY 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTGTGATGAGCTATGG 346  
 DB 1737 CACCTCCAGAACAGGAAAGATTTTATGCAAGGGCGCTCTCTTAGATGAACCTGTTG 1796  
 QY 347 AGGTGAGCAATTTCCGACCATCTACACATGTTTCATCGCTGGCCCTGTGTCTTCATCA 406  
 DB 1797 AAGTGGACCACTACAGAACATATATACATGTTTATGCGCTCCCTCATTTCTTTATCC 1856  
 QY 407 TCAGACCCCTGGGCGATCGACTTCATGATGAGGCGAGTGTGCTGGAGTTTGTGACCTAC 456  
 DB 1857 TCAGACACATTTGTAGTAGATACATGATGAGGAGGCTGGTGTGATGAGCTTCCAGCT 1916  
 QY 467 TGATCTTCAGCTTCGAGACAGTGCATTTGGCGTGGTGGTGGTGGTGGTGGTGGTGGT 526  
 DB 1917 TGTCTTAGCTTTTGGCAATTTCCATCCGTTTGGTGGTGGTGGTGGTGGTGGTGGTGG 1976  
 QY 527 CCACCCCTGTTGGCGCCCTACCGCCCTACGGCTGTGGGCGAGGGGCACTTGGACGAGG 586  
 DB 1977 CTACATTTTTCAGTTCCCTATTTCTGTTTCAACATTTGGGCGACTGGCTATAGCAAGAT 2036  
 QY 587 CGAGGGCGCTGGCTGTGCGCTTTTACGCGCCACGCGCGTGGTGTCTGCTGCGCGCTGCCG 646  
 DB 2037 CTATCCGCTGATCGGTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2096  
 QY 647 TCC-----ACGTGGCGGTGGAGCATGAGTCCCGCGCGCTCCCGTT 688



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||||| 1396 TCAACTATTATAGAACCTGGAAATGGTGGTCCATGACTGGCTATATTACTATGCTTAC 1455
QY 1222 CAGGATGGGCTGGCTCCCTTGGTCCCGGGCCGAGGGGTAGCCATGCTGGGTGTGTC 1281
Db 1456 AAGGACTTCTCTGGTTTTCTCCAGAGATTCAAATCTGCTGCCATGTTAGCTGCTTT 1515
QY 1282 CTGGTCTCCGACATGGCCATGAGTATATCTTCTGCTTGGTCTGGGTCTTCTATCCC 1341
Db 1516 GCTGTATCTCTAGTACAGGAATATGCTTGGCTGTTTGGTGGCTTTTCTATCCC 1575
QY 1342 GTCATGCTGATCTCTCTCTGTCATTGGAGGAATCTTGAATTCATGATGATGACACAG 1401
Db 1576 GTGCTCTTCTGCTCTCTATGTTCTTGGATGGCTTCACTTCAATGATGATG 1635
QY 1402 CGACCGGCGCCGATGGAACGCTGATGTGACCATGCTGTTCTAGCCAGGAATC 1461
Db 1636 CGGAAAAAGCCGATTTGGAATGTTCTGATGTGACTTCTCTTCTTGGCAATGGAGTC 1695
QY 1462 CAGGTACAGCTGACTGCCAGGAGTGTAGCCACGGCGGCACTGCCCTTACCCAGGCA 1521
Db 1696 TTACTCTGCTTTTATCTCAAGATGATGACGTCAGCTGCTCTGAAAAATCCC 1755
QY 1522 ACTTCTGGGGCTGTFGACACCTCGATCTGTTGGTCTGCTGCCAT 1563
Db 1756 ACATTTTGGATTATGTCGGCCACGTTCTCGGACTTGTGCT 1797

RESULT 11
US-60-455-444-2252
; Sequence 2252, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01455
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2252
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-455-444-2252

Query Match 25.98; Score 405.6; DB 10; Length 2738;
Best Local Similarity 58.98; Pred. No. 1.9e-86;
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

QY 287 CATCCCTGGGAAACAGAAAGTTTTCATCCGCAAGTCCCTCTGATGAGCTGATGG 346
Db 497 CACCTCCAGAACAGAAAGATTTTATTGAAGCGCTCTCTCTAGATGAACCTGTTG 556
QY 347 AGGTGACAGATTTCCGACCATCTACCATGTTTCATCGCTGGCTGTGCTCTTCATCA 406
Db 557 AAGTGGACCATCAGAACATATATACATGTTTATTGGCCCTCTCATCTCTTTATCC 616
QY 407 TCAGCACCTGCGCATCGACTTCATGATGAGGCGAGCTGCTGCTGGAGTTTGACCTAC 466
Db 617 TCAGCACACTTGTAGTATGATGATGAGGAGGCTGGTCTGAGTTTCAGCTTCC 676
QY 467 TGATCTTTCAGCTTCGACAGCTGTCATGGCTGCTGACCTGGGTGCCATGTTTCTGT 526
Db 677 TGTCTATGCTTTTGGCAAAATTCCTACCGTGTGTTGGACCTGGTGGATCATGTTCTGT 736
QY 527 CCACCTCTGTTGGCGCGTACACAGCCCTACGCTGTGGCCAGGGGCACTGGAGCGAGG 586
Db 737 CTACATTTTTCAGTTCCTATTTCTGTTTCAACATTTGGGCCACTGGCTATAGCAAGATT 796
QY 587 CGACGGCTGGCTGTGCTGCTTTTAGCGCCGCGCTGCTGCTGCGCGCTGCGCG 646
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Db 797 CTCATCCGCTGATCGTTCCTCTTCCATGGCTTCTTTTCATGATCTTCAGATTTGAG 856
QY 647 TCC-----ACGTGGCGTGGAGCATCAGCTCCCGCGCCCTCCCGTT 688
Db 857 TTCTAGGTTTGGACCAACATATGTTGTTAGATATACACTGCCACAGCTTCCCGT 916
QY 689 GTGCTCCTGCTTTCGAGCAGGTTAGTTCCTGATGAAAGCTACTCTTCTCTGAGAGAGG 748
Db 917 TCATCATTTATTCGAGCAGATTCGTTTGTAAAGAGCCCACTCATTTGTCAGAGAGA 976
QY 749 CTGTCCTGGGATCCTTCGTCGACAGCAGGTTGAGGGATCCAGCCGCCAGTTCTTCCA 808
Db 977 ACGTCCCTGGGTACTAAAT-TCAGCTAAGAGAAATCAAGCACTGTTCCCAATACATCA 1035
QY 809 G-----CTACTCTACTTCTCTCTGCCCCAACACATCATACAGGAGAGACTTACCC 861
Db 1036 GTCAACCACTATTTGACTTCTTATTTGCTCCTACCTTATCTACCGTGACAGCTATCCC 1095
QY 862 AGGAGCCCTATGTCAGGTGGAATTTATGAGCCAAAGACTTTGCCAGCCCTGGATGT 921
Db 1096 AGGAATCCCACTGTAGATGGGTTTATGCTGCTATGAAGTTTGCACAGCTCTTGGTGC 1155
QY 922 GTGCTCTATGCTGCTTCTATCCTGGCGCCCTCTGTTGTTCTCTGTTTGGCCAACTGAGC 981
Db 1156 TTTTCTATGCTACTACATCTTGAAGGCTTGTGCCCCCTTGTTCGGAATATCAAA 1215
QY 982 CGAGAGCCCTTCAGCACCCGTCGCCCTGGTGTCTCTATCTGCTGATGCCAGCTTGCAGGC 1041
Db 1216 CAGGAGCCCTTCAGCGCTGCTTCTGCTCTATGTTTAACTCCATCTTGGCAGGT 1275
QY 1042 ATCTTCATGCTGCTGCTATCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1101
Db 1276 GTGCTGATCTCTCTCTTACTTTTCTGCTTTTTCGCACTGCTGCTCAATGCCITGCT 1335
QY 1102 GAGATCTACGATTTTGAGACAGAGTGTCTTACCGGAGTGTTGGAACTCAACGCTCTTC 1161
Db 1336 GAGATCTACGCTTGTGTCAGAGATGTTCTATAAGGATTTGGTGAACCTCCACGTCATAC 1395
QY 1162 TCCAACTACTACCGACTTGGAACTGTTGGTCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1221
Db 1396 TCCAACTATATAGAACCTGGAATGTTGGTGGTCCATGCTGCTGCTGCTGCTGCTGCTG 1455
QY 1222 CAGGATGGGCTGCGCTCTCTTGGTGGCGGCGGAGGGGTAGCCATGCTGGGTGTGTTTC 1281
Db 1456 AAGGACTTCTCTGGTTTTTCTCCAGAGATTCAAATCTGCTGCCATGTTAGCTGCTTT 1515
QY 1282 CTGCTCTCCGAGTGGCCCATGAGTATATCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 1341
Db 1516 GCTGTATCTCTCTAGTACAGGAATATGCTTGGCTGTTTGGTGGCTTTTCTATCCC 1575
QY 1342 GTCATGCTGATCTCTCTTGTGTCATTGGAGGAATGTTGAACCTTCATGATGATGACACAG 1401
Db 1576 GTGCTCTTCTGCTCTCTATGTTCTTGGAAATGGCTTCACTTCAATGATAGT 1635
QY 1402 CGCACCGCCCGGATGGAACGCTGCTGATGAGCAATGCTGTTCTAGGCCAGGAATC 1461
Db 1636 CGGAAAAAGCCGATTTGGAATGTTCTGATGGAATGCTTCTTCTTGGCAATGGAGTC 1695
QY 1462 CAGGTACGCTGACTGCCAGGAGTGTAGCCAGGCGGCACTGCCCTTACCCAGGCA 1521
Db 1696 TTACTCTGCTTTTATCTCAAGATGTTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1755
QY 1522 ACTTCTGGGGCTGTTGACACCTTCGATCTTGGTCTGCTGCCAT 1563
Db 1756 ACATTTTGGATTATGTCGGCCACGTTCTCGGACTTGTGCT 1797
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RESULT 12  
US-60-452-680-8056  
; Sequence 8056, Application US/60452680  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: GRUPE, Andrew

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/60/452,680  
; NUMBER OF SEQ ID NOS: 116213  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8056  
; LENGTH: 2738  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-452-680-8056

Query Match 25.9%; Score 405.6; DB 11; Length 2738;  
Best Local Similarity 58.9%; Pred. No. 1.9e-86;  
Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

Qy 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGAAAGTCCCTGCTGTAGATGAGTGTATGG 346  
Db 497 CACCTCCAGAACAGGAAGATTTTATTCGAAGCGCTCTCTCTAGATGAAGTGTGCTTGG 556  
Qy 347 AGGTGCAGCATTTCCGACCATCTACACATGTTTCATCGCTGGCTGTGTCTCTTCATCA 406  
Db 557 AAGTGGACCATCAGAACATATACATGTTTATTGGCCCTCTCATCTCTTTATCC 616  
Qy 407 TCAGCACCTTGGCCATCGACTTCATGATGAGGAGGCTGCTGTGAGTTTGACCTAC 466  
Db 617 TCAGCACATCTGTAGTAGATTACATTTGATGAAGGAGGCTGTGTGAGTTTGACCTCC 676  
Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGTGTGACCTGGCTGCCATGTTTCTGT 526  
Db 677 TGTCTTATGCTTTTGGCAAAATTTCTACCGTGTGTGGACCTGGTGGATCATGTTCTGT 736  
Qy 527 CCACCTGTTGGCCCGTACAGGCCCTACGGCTGTGGCCAGGGGACCTGGAGCGAG 586  
Db 737 CTACATTTTCAGTTCCTTATTTCTGTTTCAACATTTGGGCCACTTGGCTATAGCAAGAGT 796  
Qy 587 CGAGCGGCTGGGTGTGCGCTTTTAGCGCCACCGCTGTGTGCTCTGCGCGCTGCCGG 646  
Db 797 CTCATCCGCTGATCGTCTCTCTCCATGCGCTTTCTTTTCATGATCTTCCAGATTGGAG 856  
Qy 647 TCC-----ACGTGGCGTGGAGCATCAGCTCCCGCGCGCTCCCGTT 688  
Db 857 TTCTAGGTTTTGGACCAACATATCTGTGTAGCATATACACTCCACAGCTTCCCGGT 916  
Qy 689 GTGCTCTGCTTCGAGCAGGTAGTGTCTGATGAAAGCTACTCTCTCTGAGAGAGG 748  
Db 917 TCATCATATATTCGACGAGATTCGTTTGTATGAAGGCCCACTCATTTGTCAGAGAGA 976  
Qy 749 CTGTCCTGGGATCCTTGTGCCAGAGAGGTGAGGGGATCCAGGCCCGCCAGTTTCTCCA 808  
Db 977 ACGTGCCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTTCCAAATACCTACA 1035  
Qy 809 G-----CTACCTCTACTCTCTCTTGGCCCAACATCATCTACAGGAGACTTACCCT 861  
Db 1036 GTCAACAGCAATTTGTACTTCTTATTTGCTCTTACCTCTATCTACCGTGTGACAGCTATCC 1095  
Qy 862 AGGAGCGCTATGTCAGTGAATATGTGCGCAAGAACTTTCAGGCGCTTGGAGGT 921  
Db 1096 AGGAATCCCACTGTAAAGTGGGTATGTGCTGTATGAAGTTTGCACAGGTTCTTGGTTGC 1155  
Qy 922 GTGCTCTATGCTCTCATCTGGCGCGCTCTGTGTCTGTCTGTCTTGGCCAAATGAGC 981  
Db 1156 TTTTCTATGTGTACTACATCTTTGAAAGGCTTTGTGCGCCCTTGTTCGGAATATCAA 1215  
Qy 982 CGAGAGCCCTTCAGACCGCTGGCTGTCTCTATCTATCTGATGCCAGCTTGGCCAGGC 1041  
Db 1216 CAGGAGCCCTTCAGCGCTCGTGTCTGTGCTCTATGTGATTTAACTTCACTCTTGGCAGGT 1275  
Qy 1042 ATCTTCATGCTGCTCATCTCTTTCCTCTTCCATCTGCTGCTCAAGCGCTTGGC 1101  
Db 1276 GTGCTGATCTCTCTTACTTTTTTGGCCCTTTTGGCACTGCTGGCTCAATGCTCTTGT 1335

## RESULT 13

US-60-453-135-4736

; Sequence 4736, Application US/60453135

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: IAKOUBOVA, Olga

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001456

; CURRENT APPLICATION NUMBER: US/60/453,135

; CURRENT FILING DATE: 2003-03-10

; NUMBER OF SEQ ID NOS: 82762

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4736

; LENGTH: 2738

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-453-135-4736

Query Match

25.9%; Score 405.6; DB 11; Length 2738;

Best Local Similarity 58.9%; Pred. No. 1.9e-86;

Matches 767; Conservative 0; Mismatches 509; Indels 26; Gaps 3;

Qy 287 CATCCCTGGGGAACAGAAAGTTTTCATCATCCGAAAGTCCCTGCTGTAGATGAGTGTG 346  
Db 497 CACCTCCAGAACAGGAAGATTTTATTCGAAGCGCTCTCTCTTAGATGAAGTGTG 556  
Qy 347 AGGTGCAGCATTTCCGACCATCTACACATGTTTCATCGCTGGCTGTGTCTTCATCA 406  
Db 557 AAGTGGACCATCAGAACATATACATGTTTATTGGCCCTCTCATCTCTTTATCC 616  
Qy 407 TCAGCACCTTGGCCATCGACTTCATGATGAGGAGGCTGCTGTGAGTTTGACCTAC 466  
Db 617 TCAGCACATCTGTAGTAGATTACATTTGATGAAGGAGGCTGTGTGAGTTTGACCTCC 676  
Qy 467 TGATCTTCAGCTTCGGACAGCTGCCATTTGGCGCTGTGTGACCTGGCTGCCATGTTTCTGT 526  
Db 677 TGTCTTATGCTTTTGGCAAAATTTCTACCGTGTGTGGACCTGGTGGATCATGTTCTGT 736  
Qy 527 CCACCTGTTGGCCCGTACAGGCCCTTACGGCTGTGGGCCAGGGGACCTGGAGCGAG 586









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